Page 1

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GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on:

December 12, 2003, 02:59:14 ; Search time 80 Seconds (without alignments) 5128.796 Million cell updates/sec

US-09-617-099B-1 82B5 1 MSAPLGPRGRPAPTPAASQP.....TRRASQSSLESSTGPSYSRS 1590

Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

830525 seqs, 258052604 residues Searched:

830525 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

sp. vertebrate:*
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ALIGNMENTS

RESULT 1

PROSITE; PS50004 PROSITE; PS00190 PROSITE; PS50106	SMART; SM00228; PDZ; 1. PROSTWE. PSECOOM. C2 POWATE	Pfam, PF00595; P SMART; SM00239;	Pfam; PF00168; C2; 2.	DR InterPro; IPR001478; PDZ. DR InterPro; IPR000306; 2nf PYVR	InterPro; IPR000345;	InterPro; IPR000008;	MGD; MGI:2	HSSP; P21707; 1B	EMBL; AB021131; BAB18975.1;	CC -1- SIMILARITY: CONTAINS 1 PDZ/DHR DOMAIN.	-1- SIMILARITY: CONTAINS 2	Nat. Cell Biol. 2	"CAMP-GEFII is a direct target of CAMD in remilated and	Sunaga Y., Yano H., Matsuura Y., Twanaga T.	Ozaki N., Shibasaki T., Kashima V. Miki T. makahamki w	AF SEQUENCE FROM N.A. BY MENTINESCOTORS D. T. H. M. A. 1.1.05 from		NCBI TaxID=10090;	<pre>UC Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; OC Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murine. M.</pre>	Mus musculus (Mouse).		Rim2.	01-MAR-2003 (TrEMBLrel.	OI MAD SOUTH (PROMOTES TO)	At Land Annual Contracts	AD COROLL PRELIMINARY; PRT; 1530 AA.		O9BO27
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RP SEQUENCE FROM N.A.

RP ABGUINCE FROM N.A.

RA MEDLINE-20347919; PubMed-10748113;

RA MEDLINE-20347919; PubMed-10748113;

RA MEDLINE-20347919; PubMed-10748113;

RA MEDLINE-20347919; PubMed-10748113;

RT ABAB and a new class of Src homology 3 domain proteins.";

RL J. Biol. Chem. 275:2003-2004 (2000).

CC -1- SIMILARITY: CONTAINS 1 PDZ/DHR DOMAIN.

CC -1- SIMILARITY: CONTAINS 2 C2 DOMAINS.

CC -1- SIMILARITY: CONTAINS 2 C2 DOMAINS.

BRED: A2199331; AAP81653.1; -.

DR EMED: P21707; 1BYN.

InterPro; IPR001049; C2.

DR InterPro; IPR001418; PDZ.

DR InterPro; IPR001315; RPH3A effector.

DR InterPro; IPR001306; Znf_FYUR.

DR Pfem; PF00168; C2; 2.

PF6m: DF00168; C2; 2.
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Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus
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                                    Gaps
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       Length 1530;
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       DB 11;
   Score 7930; DE Pred. No. 0; Mismatches
   95.7%;
Query Match
Best Local Similarity 96.2
Matches 1529; Conservative
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MEDLINE=20347919; PubMed=10748113;

WANG Y., Sugita S., Sudhof T.C.;

"The RIM/NIM Family of Neuronal C2 Domain Proteins. Interactions with
Rab3 and a new class of Sct. Domology 3 domain proteins.";
J. Biol. Chem. 275:20033-20044(2000).
-!- SIMILARITY: CONTAINS 2 C2 DOMAINS.
-!- SIMILARITY: CONTAINS 1 PDZ/DHR DOMAIN.

EMBL; AR199330; AAPR1652.1; -.

HSSP; P21707; 1BYN.

InterPro; IPR000008; C2.

InterPro; IPR000345; CytC_heme_bind.
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                                                                                                                                Gaps
                                                                                                    DB 11; Length 1525;
                                                                                                                                30; Indels 109;
SMART; SM00228; PDZ; 1.

PROSITE; PS50004; CZ DOMAIN 2; 2.

PROSITE; PS50106; CTTCCHROWE C; 1.

PROSITE; PS50106; PDZ; 1.

PROSITE; PS50178; ZF FYVE; 1.

SRQUENCR 1525 AA; 172435 MM; D4930D5DZF03CF21 CRC64;
                                                                                                 90.0%; Score 7459.5;
90.1%; Pred. No. 0;
ive 21; Mismatches
                                                                                                              Best Local Similarity 90.18 Matches 1452; Conservative
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Best Local S
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                                                                                                                                                                                                                                      1345 BASQLEQTEGGGRELRSTVQRSTETCLAVEMENNMTRQASEESTDGGMRSYESECHLIFP
11294 BASQLEGTEGGGRELRSTVQRSTETGLAVEMENNMTRQASRESTDGSMRSYSBEGGLIFP
                                                 754 LPSREDGRPRNPYVKIYFLPDRSDKNKRRTKTVKKTLEPKNNGTFIYSPVHRREFRERM.
                                                                                              BITIMDARVREEBSRFJARILIELETALLDDEPHWYLQTHDV88LFLPRBSPYLPRRO
                                                                                                                    814 BITLWDQARVREBESSFLGBILIBLETALLDDSPHWYKLQTHDVSSLPLPHPSPYMPRRQ
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                           LPSREDGRPRNPYVKI YFLPDRSDKNKRRTKTVKKTLBPKNNOTFI YSPVHRREFRRML
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
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                                                                                                                                                                                                                                                                                          31; Indels 123;
| InterPro; IPR001478; PDZ. | InterPro; IPR003315; RPHJA_effector. | InterPro; IPR000305; Znf_FTVE. | InterPro; IPR000305; Znf_FTVE. | InterPro; IPR001080; Znf_FTVE. | Pfam; PP00168; CZ; 2. | Pfam; PP00168; CZ; 2. | Pfam; PP00129; DZ; 1. | PR001718; RMART; SM00228; PDZ; 1. | RMART; SM00228; PDZ; 1. | RMART; SM00228; PDZ; 1. | RROSITE; PS50109; CTPCHROME_C; 1. | RROSITE; PS50109; CTPCHROME_C; 1. | RROSITE; PS50109; ZTFYE; 1. | RROSITE; PS50109; ZTFYE; 1. | RROSITE; PS50108; ZE_FYE; ZE_FY
                                                                                                                                                                                                                                                     19.8%; Score 7438.5; larity 89.2%; Pred. No. 0; Conservative 21; Mismatches
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MEDLINE=20347919; PubMed=10748113;
Wang Y., Sugita S., Sudhof T.C.;
"The RIN/NIM Family of Neuronal C2 Domain Proteins. Interactions with
Rab3 and a new class of Src homology 3 domain proteins.";
J. Biol. Chem. 275:2003-20044(2000).
-1- SIMILARITY: CONTAINS 2 C2 DOMAINS.
-1- SIMILARITY: CONTAINS 1 PDZ/DHR DOMAIN.
BMBL; AR199322; AAF81644.1;
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                                                                                                                          InterProj IPRO00345; CytC heme_bind.
InterProj IPRO01478; PDZ._
InterProj IPRO01345; CytC, heme_bind.
InterProj IPRO01345; RPH3A effector.
InterProj IPRO0136; Znf_FYVB.
R Ffam; PPO0168; C2; 2.
R Ffam; PPO0158; PDZ, 1.
R SWART; SW00228; PDZ, 1.
R SWART; SW00228; PDZ, 1.
R RROSITE; PS00190; CYTOCHROWE_C; 1.
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                                                                   SKKGGKWRQVSLSSSEEKLASTPRYTSCDDVKLESESVSEKGDSQKGKRKTSEQGVLSDS
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RX MAD Y., Sugita S., Suddhof T.C.;
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DR RIGEPRO; IPRO0008; C2.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI _TaxiD=10116;
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Wang Y., Sudita S., Sudhof T.C.;
Wang Y., Sudita B., Sudhof T.C.;
Wang Y., Sudita B., Sudhof T.C.;
Wang Y., Sudita Panily of Neuronal C2 Domain Proteins. Interactions with
Rab3 and a new class of Ser homology 3 domain proteins.";
J. Biol. Chem. 275:20033-20044(2000).
-!- SIMILARITY: CONTAINS 2 C2 DOMAINS.
-!- SIMILARITY: CONTAINS 1 PDZ/DHR DOMAIN.
EMBL, AR199329; AAR81651.1;
-- HSSP; P21707; 1BYN.
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                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI TaxID=10116;
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ILLDELELSNAVIGWFKLFPPSSLVDPTLAPLTRRASQSSLESSTGPSYSRS 1399
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PROSITE; PS50178; ZF FYVE; 1.
SEQUENCE 1330 AA; 151045 MM; 485906B1F668FC73 CRC64;
                                                                                                                    Created)
Last sequence update)
Last annotation update)
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                                                                                     PRT; 1330 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Interpro; IPR000008; C2.
InterPro; IPR000345; CytC_heme_bind.
InterPro; IPR001478; PDZ.
InterPro; IPR003315; RPH3A_effector.
InterPro; IPR000306; Znf_FYVB.
Pfam; PF00168; C2; 2.
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Pfam; PF0318; RH3A effector; 1.
SMART; SM00239; C2; 2.
SMART; SM00228; PDZ; 1.
PROSITE; PS50004; C2 DOMAIN 2; 2.
PROSITE; PS00190; CYTOCHROME C; 1.
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                                                                                     PRELIMINARY;
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RA MEDLINE=20347919; PubMed=10748113;

RA MEDLINE=20347919; PubMed=10748113;

RT RAD3 and a new class of Src homology 3 domain proteins. ";

L. SIMILARITY: CONTAINS 1 PDZ/DRR DOWAIN.

CC -1- SIMILARITY: CONTAINS 2 C2 DOWAINS.

DR RMEL; AR199322; AAP81648.1; -.

DR RMEL; AR199325; AAP81648.1; -.

DR RMEL; AR199326; AAP81648.1; -.

DR RMEL; AR199327; AAP81648.1; -.

DR RMEL; AR199327; AAP81649.1; -.

DR RMETPRO; IPRO000345; C2.

DR PEAM; PRO0168; C2; 2.

DR PEAM; PRO018; C2; 2.

DR PEAM; PRO018; C2; 2.

DR SWART; SM00239; C2; C2 DOWAIN 2; 2.

DR PROSITE; PS50109; CTTOCHOMĒC; 1.

DR PROSITE; PS50106; PDZ; 1.
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                                                                    1241 LYQQLLSFERSPQGKVLQIIVWGDYGRMDHKSFMGVAQILLDELELSNWVIGWFKLFPPS
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                                  LYQQLLSFEESPQGRVLQIIVWGDYGRMDHKSFWGVAQILLDELELSNMVIGWFKLFPPS
                                                                                                                                                                                                                                                                                                                                                                                        Q9JHJ6;
01-OCT-2000 (TYENBLrel. 15, Created)
01-OCT-2000 (TYENBLrel. 15, Last sequence update)
01-OCT-2000 (TYENBLrel. 23, Last annotation update)
01-MAR-2003 (TYENBLrel. 23, Last annotation update)
RIM2-5C (RIM2-2A) (RIM2-3B) (RIM2-4A).
RIM2-5C (RIM2-2A) (RIM2-3B) (RIM2-4A).
Battus norvegicus (Rat).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
(11)
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                                                                                                                                                     SLVDPTSAPLTRRASQSSLESSTGPSYSRS 1590
                                                                                                                                                                                       SLVDPTLAPLTRRASQSSLESSTGPSYSRS 1330
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Db 1116GGGKK 1120	QY 1359 IRSTVQRSTETGLAVERRNWHTRQASRESTDGSMNSYSSEGNLIFFGVRLASDSQFSDFL 1418	CY 1419 DGLGPAQLVGRCTLATPAMGDIGVGAMDKRGQLRVEIIRARGLVVKPGSKTLPAPVXKVY 1478	OY 1479 ILDNGVCIAKKTIKVARKTLEPLYQQLLSFEESPQGRVLQIIVWGDYGRMDHKSFMGYAQ 1538 	QY 1539 ILLDELELSNMVIGWPKLPPPSSLVDPTSAPLTRRASQSSLESSTGPSYSRG 1590 	RESULT 8 Q9JIR9 DPRLIMINARY: PRT: 1368 AA	Q9JIR9; 01-0CT-2000 (TERMBLRel. 15, Created) 01-0CT-2000 (TERMBLRel. 15, Last sequence 01-MAR-2003 (TERMBLRel. 23, Last semontal.	DE RIM2-3A. GN RIM2-3A. GN RIM2-3A. CS Rattus norvegicus (Rat). CC Rikarvola: Metazoa. Charists. Vertebrats. Fittel content.			RL J. Biol. Chem. 275:20033-20044(2000). CC -1-SIMILARITY: CONTAINS 1 PDZ/DHR DOMAIN. CC -1-SIMILARITY: CONTAINS 2 C2 DOMAINS. DR FMRT: APPROACE: AMERICA 1.	HSSP; P21707; IRSY. INCETPTO; IPROMODOB; C2. INCETPTO; IPROMODOB; C2. INCETPTO; IPROMODA45; CYC. he INCETPTO; IPROMODA478; PDZ.	DR InterPro; IPR003315; RPH3A_effector. DR InterPro; IPR000306; Znf_FYVB. DR Pfam; PF00169; C2; 2. DR Pfam; PF00595; PD2; 1.	Pfam; PF02318; RPH3A effectc SWART; SW00239; C2; Z SWART; SW00228; PDZ; 1. PROSITE; PS50004; C2 DOMAIN	DR PROSITE; PS00190; CYTOCHROME C; 1. DR PROSITE; PS50106; PDZ; 1. DR PROSITE; PS50176; ZF FYVF; 1. SQ SRQUENCE 1368 AA; 155560 MW; CE08E16F0B383A11 CRC64;	Duery Match 78.5%; Score 6504; DB 11; Sest Local Similarity 78.9%; Pred. No. 0; Atches 1283; Conservative 18; Mismatches 29;	APLGPRGRPAPTPAAGOPPOPEMPDLSHLTBERKIILAVDROKGEBKBGSVLKI 60	KEEHKAQPTQWPPFSGITELVNNVLQPQQXQPNEKEPQTKLHQQPEMYKEQVKXMGEESQ	П

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                                                                             SRISLIRNDR PGRORSVSERRAAMENORSYSMERTREAQGOGSTPORTSPFTERESP
                                                                                                                                                                                                                                                                                                     501 SKKGGROMRQVSLSSSBEBILASTPRYTSCDDVBIBSBSVGRKGDDMB------
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1083 ROASRESTDGSMNSYSSEGNLIFFGVRLASDSGFSDFLDGLGPAGLVGRGTLATFAMGDI
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RN [1]

RN [1]

RX MART; SUGILER S., Sudhed=10748113;

RA MART; SUGILER S., Sudhed=10748113;

RA MART; SUGILER S., Sudhed T.C.;

RAD3 and a new class of Src homology 3 domain proteins.";

L. SHMILARITY: CONTAINS 2 C2 DOMAINS.

CC -! - SIMILARITY: CONTAINS 1 P2Z/DHR DOMAIN.

DR REMEL; AR19328; AAR81650.1; -.

DR REMEL; AR19328; AAR81650.1; -.

DR REMEL; AR19328; AAR81650.1; -.

DR RICEPPO; IPRO01045; Cyt_heme_bind.

DR InterPro; IPRO0345; Cyt_heme_bind.

DR InterPro; IPRO0346; Znf_FYVR.

DR RICEPPO; IPRO0356; Znf_FYVR.

DR PROS18; P8D2; 1.

DR SMART; SM00239; P2Z; 1.

DR SMART; SM00239; P2Z; 1.

DR PROSITE; PSS5004; CZ DOMAIN 2; 2.

DR PROSITE; PSS5016; P2Z; 1.

DR PROSITE; PSS50178; ZF_FYVR; 1.

SROURNCR 1292 AA; 146933 MW; R15B2C2B25452094 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   200
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QQQRQKQDAPTCGICHKTKFADGCGHNCSYCQTKFCARCGGRVSLRSNKVMWVCNLCRKQ 140
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 KBEHKAQPIQWFPFSGITELVNNVLQPQQKQPNEKEPQTKI.HQQPEMYKEQVKKWGEESQ 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   241 VEKGRAHGIJTRODTIKNGSGVIGHQIASDMPSDRKRSPSVSRDQNRRYEQSEEREDYSQYV 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PSDGTMPRSPSDYADRRSQRRPQFYEEPGHLNYRDSNRRGHRHSKEYIVDDEDVESRDEY 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 361 ERQRREBEYQARYRSDPNLARYPVKPQPYEEQMRIHAEVSRARHERRHSDVSLANAELED 420
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MSAPLGPRGRPAPTPAASQPPPQPEMPDLSHLTBEBRKIILAVMDRQKKBBEKEQSVLKI
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                                                                                                                                                                                                                                                                                                            Rattus norvegicus (Rat).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
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LDBLELSNWVIGWFKLFPFSSLVDFTLAPLTRRAGQSSLESSTGPSYSRS
                                                                                                                                                                                            Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 75.0%; Score 6212; DB 11; Best Local Similarity 77.1%; Pred. No. 0; Matches 1226; Conservative 21; Mismatches 45;
                                                                                                                                                   1292
                                                                                                                                                                                            01-OCT-2000 (TrEMBLrel. 15,
01-OCT-2000 (TrEMBLrel. 15,
01-MAR-2003 (TrEMBLrel. 23,
                                                                                                                                                 PRELIMINARY;
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RIM2-4B.
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                                                                                            RESULT 10
29JIRB
1D 20JIRB
1D 01-0C
DT 01-NC
DT 01-NC
DT 01-NC
DT 01-NC
DT 01-NC
DR RIM2-
OS RATTU-
OS REBLI,
DR 111c-
DR 1
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573 LESESVSEKGDSQKGKRKTSEQGVLSDSNTRSERQKKRMYTGGHSLERDLEWSEDQIKDS 632
341 IESESVSEKGDSQKGKRKTSEQAVLSDSNTRSERQKEMYFGGHSLERDLEWSEPQIKDS 400
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Q9JIR4
ID Q9JIR4
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TISSUE Brain;

TISSUE Brain;

MATHER TO, SUDAMED B., KIKUMO R., MIYajima N., Tanaka A.,

MEDINING-9089487; PubMed-9872452;

MEDINING-9089487; PubMed-9872452;

MATHER T., Ishikawa K., Suyama M., Kikumo R., Miyajima N., Tanaka A.,

MATHER T., Ishikawa N., Ohara O.;

MATHER T., Ishikawa N., Ohara O.;

MATHER T., Orange Braylences of unidentified human genes. XI.

MATHER T., The complete sequences of 100 new cDNA clones from brain which code

RT The complete sequences of 100 new cDNA clones from brain which code

RT The COMPLIANTY: CONTAINS 1 PPZ/DHR DOMAIN.

CC -1- SIMILARITY: CONTAINS 2 C2 DOMAINS.

MATHER PRO1829; MAX-4471.1; -.

MATHER TOO 1 PRO00008; C2.

MATHER TOO 1 PRO00108; PDZ; 1.

MATHER TOO 1 PRO0228; PDZ; 1.

MATHER TOO
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 QVGMMDKKGQLEVEIIRARGLVVKPGSKTLPAPYVKVYLLDNGVCIAKKKTKVARKTLEP 1202
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       41 RKRSPSVSRDQNRRYDQNRERREFYSQYATSDTAMPRSPSDYADRRSQHEPQFYEDSDHLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     METHAEVSRARHERRHSDVSLANADLEDSRISMLRMDRPSRQRSISERRAAMENQRSYSM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   273 RKRSPSVSRDQNRRYEQSEEREDYSQYVPSDGTMPRSPSDYADRRSQREPQFYEEPGHLN
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                                   LYQQLLSFERSPQGRVLQIIVMGDYGRMDHKSFMGVAQILLDRLELSNMVIGWFKLFPPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 83.3%; Fred. No. v.,
Matches 1099; Conservative 24; Mismatches 23; Indels 174; Gaps
                                                                                                                                                                                                                                           01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAX-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical protein KIAA0751.
KIAA0751.
Homo saplens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCB1. TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 4; Length 1188;
                                                                                                           SLVDPTSAPLTRRASQSSLESSTGPSYSRS 1590
                                                                                                                              SLVDPTLAPLTRRASQSSLESSTGPSYSRS 1292
                                                                                                                                                                                                                                       PRT; 1188 AA
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Pred. No. 0;
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83.3%;
                                                                                                                                                                                                                                     PRELIMINARY;
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Best Local Similarity
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Q9UQ26;
01-MAY-2000 (
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090026
10 090026
AC 09002
AC 09002
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BD Hypot
BD Hypot
GN Mamma
OX NCB1
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RX MEDLI
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RY TOT
RY TEC
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CC -1-5
CC -1-5
CC -1-5
DR BMBL
DR HSSP
DR Gener
DR Inter
DR Inter
DR Inter
DR Inter
DR SWAR
DR SWAR
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1110 1170 1008 1470 1128 1188 1009 DSQPSDFLDGLGPAQLVGRQTLATPAMGDIQVGMMDKKGQLEVEIIRARGLVVKPGSKTL 1068 993 VSDYRHNGRDLQSSTLSVPBQVMSSNHCSPSGSPHRVDVIGRTRSMSPSAPPPQ-RNVBQ 1051 1171 QLPPKGTLERSAMDIBERNRQMKLNKYKQVAGSDPRLEQDYHSKYRSGWDPHRGADTVST 1230 1291 TKSTSISGDMCSLEKNDGSQSDTAVGALGTSGKKRRSSIGAKMVALVGLSRKSRSASQLS 1350 1471 PAPYVKVYLLDNGVCIAKKKTKVARKTLBPLYQQLLSFBBSPQGRVLQIIVMGDYGRMDH 1530 KSFMGVAQIILIDELEISNMVIGWFKLFPPSSLVDPTSAPLTRRASQ8SLESSTGPSYSRS 1590 820 880 940 1231 KSSDSDVSDVSAVSRTSSASRFSSTSYMSVQSERPRGNRKISVFTSKMQNRQMGVSGKNL 1290 992 760 460 521 PEPQVELVVSRPIGDIPRIPDSTHAQLESSSSSPRSQMORPSISVTSPWSPGMLRDVPQ 580 872 752 VGGRATESGRICAPITKVKKGSLADTVGHIRPGDEVLEMNGRLIQGATFEEVYNIILESK 520 873 VKKTLEPKWNQTFIYSPVHRREFRERMLEITLADQARVRERESEFIGBILIELETALLDD 932 761 VSDYRHDGRDLQSSTLSVPRQVMSSNHCSPSGSPHRVDVIGRIRSWSPSVPPPQSRNVBQ ---GGKKLRSTVQRSTETGLAVEMENWITRQASRESTDGSMRSYSBEGKLIFPGVRLAS 1069 PAPYVKVYLLDINGVCIAKKKTKVARKTLEPLYQQLLSFERSPQGKVLQIIVMGDYGRMDH KSFWGVAQILLDELELSNAVIGWFKLFPPSSLVDFTLAPLTRRASQ88LESSTGPSYSRS 813 FLSGQLSIKLWFDKVGHQLIVTILGAKDLPSREDGRPRNPYVKIYFLPDRSDKWKRRTKT 641 VKKTLEPKWNOTFIYSPVHRREFRERMLEITLWDQARVRERSEFLGEILIKLETALLDD GIRGIRIWICHYNTI SRMDRHRVMDHYSPORDRDCGAADRQPYHRSRSTEQRPLLIRRTT TRSRSSERPDTNI-MRSMPSI-MTGRSAPPSPALSRSHPRTGSVQTSPSSTPGTGRRGRQLP 1351 QTEGGGKKLRSTVQRSTETGLAVEARNWMTRQASRESTDGSMNSYSSEGWLIFPGVRLAS GYDTCSSTTLAREHSHSDKHPYTWQPSKDGDRLIGRILLAKRLKDGSVPRDSGAMLGLKV 1052 GHRGTRA-TGHYNTISRMDRHRVMDDHYSSDRDRDCRAADRQPYHRSRSTBQRPLLERTT DSQPSDFLDGLGPAQLVGRQTLATPAMGDIQVGMMDKKGQLRVRIIRARGLVVKPGSKTL GVDTCSSTTTLNBEHSHSDKHPVTWQPSKDGDRLIGRILLNKRLKDGSVPRDSGAMLGLKV S81 FLSGQLSIKLWFDKVGHQLIVTILGANDLPSREDGRPRNPYVKIYFLPDRSDKNRRRKTKT VGCKMTESGRI.CAPITKVKKGSLADTVGHLRPGDEVLEMNGRILLQGATFREVYNIILESK 753 PEPOVELVVSRPIGDIPRIPDSTHAQLESSSSSFRSQKWDRPSISVTSPMSPGMLRDVPQ 941 QLPPKGTLDRKA------

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1097 SRKGTASDADRVLPPCLSRRGYATPRATDQPVVRGKYPTRSRSSERSSYRTLCSWHHLAP 1156
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                                                                                                                               616 HSLEEDLEWSEPQIKDSGVDTCSSTTLNEEHSBKHPVTWQPSKDGDRLIGELLLNKRL 675
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                                    382 MLARYPVKAPPEROQMEMEARVSRAKHERRHSDVALDHTE-------AAAAAP
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REDILNE-20347919; PubMed-10748113;

RM MAND Y., Sugites A., Suddhof T.C.;

MAND Y., Sugites A., Suddhof T.C.;

RT Rab3 and a new class of Src homology 3 domain proteins. i,

The RIMINARM Family of Neuronal C2 Domain Proteins with

RT Rab3 and a new class of Src homology 3 domain proteins.";

The RIMINARITY: CONTAINS 2 C2 DOMAINS.

C. -! - SIMILARITY: CONTAINS 1 PDZ/DHR DOMAIN.

DR REAL; AR199333; AAF81655.1; -.

RIGEL; AR199333; AAF81655.1; -.

RIGEL; AR199333; AAF81655.1; -.

BR INTERPRO; IPRO0194; ATPase_a/bcentre.

BR INTERPRO; IPRO0194; ATPase_bind.

RIMINARITY: SNO01345; CTC_heme_bind.

RIMINARITY: SNO0135; CZ; 2.

BR INTERPRO; IPRO0136; Znf_FYVE.

BR Ffam; PPO0168; CZ; 2.

BR Ffam; PPO01595; PDZ; 1.

BR FRANT; SNO0239; PDZ; 1.

BR FRANT; SNO0239; PDZ; 1.

BR ROSITE; PSO0104; C2 DOMAIN 2; 2.

BR ROSITE; PSO0104; C2 DOMAIN 2; 2.

BR ROSITE; PSO0104; C2 DOMAIN 2; 2.

BR ROSITE; PSSO104; C2 DOMAIN 2; 2.

BR ROSITE; PSSO104; DZ; ATPASE ALPHA BETA; 1.

BR ROSITE; PSSO105; PDZ; 1.

BR ROSITE; PSSO
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                                                                                                                                         Rattus norvegicus (Rat).
Bukaryota, Metazoa; Chordata, Craniata, Vertebrata, Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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54.5%; Score 4513.5; DB 11; Length 1615;
Best Local Similarity 55.7%; Pred. No. 2.4e-274;
Matches 961; Conservative 208; Mismatches 312; Indels 243;
                          Created)
Last sequence update)
Last annotation update)
                          23,
                      01-OCT-2000 (TrEMBLrel.
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01-MAR-2003 (TrEMBLrel.
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Db 117 QVRKIGKBARRYQGEHKDDAPTCGICHKTKFADGCGHLCSYCRTKFCARCGGRVSLRSNN 176	OY 170VANVCKI_CRKQQEILIKSGAMFYNSGSNTLQQPDQKVPRGLKNBEAPOR 218	OY 219 KKAKLHBOPOPOGAPODLSVPAVEKGRAHGLTRODTIKNGS	QY 264 QIASDMPSDRIKRSPSVSRDQNRRYRQSERREDYSQYVPSDGIMPRSPSDYADRR 317	QY 318 SQREPQFYEEPGHLAYRDSNRRGHRHSKEYIVDDEDVESRDEYERQRREEEYQARYRSDP 377	OY 378 NLARYPVKOOPYEEGMRIHAEVSRARHERRHSDVSLANAELEDGRISLLRMDRFSRGRSV 437	CY 438 SERRAAMENORSYSMERTREACGGSSTPCRTSKHSPPTPRRSPIPLDRPDMRADDSLRKQ 497 1	OY 498 HHLDPSSAVRKTKREKMETMLRNDSLSSDQSESYRPPPFRPRKKKKGGKNRQVSLSSS 555	QY 556 REBLASTPEYTSCDDVELSSESVSEKGDSQKGKRKTSERQGVLSDSNTRSERQKGRRYYGG 615 DD 548 KERGVSTPEYTSCEDVELSBSSVSEKGDLDYY 579	OY 616 HSLEEDLEWSEPQIKDSGVDTCSSTTLAREHSHSDKHPVTWQPSKDGDRLIGRILLAWRL 675	QY 676 KDGSVPRDSGAMLGLKVVGGRATTSGRLCAPITKVKKGSLADTVGHLRPGDEVLEMNGRL 735 	QY 736 LQCATFEEVYNIILESKPEDQVELVVSRPIGDIPRIPDSTHAQLESSSESFESQKWDRPS 795	OY 796 ISVTSPMSPCHLRDVPOFLSGOLSİKLMFDKVGHQLIVTILGAKDLPSKEDGRPRNPYVK 855	Qy 856 IYFLPDRSDRNKRRTKTVKKTLEPKWNQTFIYSPVHRREFRERMLEITLMDQARVREES 915 	OY 916 EFLGELLIELETALLDDEPHWYKLQTHDVSSLPLPRPSPYLPRRQIHGESPTRRLGRSKR 975	OY 976 ISDSEVSDYDCEDGYGVV9DYRHNGRDLQSSTLSVPEGVMSSNHCSP8GSPHRVDVIG 1033	QY 1034 RIRSWEPSAPPORNVEQCHRCTRAIGHYWIISRMDRHRWADDHYSSDRDCEA 1088 DD 978 RPRSRLPNV-PLQRSLDSIHPTRRSRSPTRHHDAGRRSPADHRSRHWEGQYSSEPDSELLM 1036	QY 1089 ADRQPYHRSRSTEQRPLILERTTTRSRSSERPDTNLMESMPSLMT 1132 DD 1037 LPRAKRGRSABSLHMTSELQPSLDRARSASTWCLRPDTSLHSPERERHSRKSERCSIQKQ 1096	Qy 1133 GRSAPPSPALSRSHPRTGSVQTSPSSTPGTGRRGRQLPQLPPR-GTLERSAMDIEERNRQ 1191
Db 1393 TETGWAARWRK-WVRQPSRESTNGSINSYSSEGNIIFPGVRVGPDSQFSDFLDGJGDAQL 1451	NGVCI 1486	AKKKTKVARKTLEPLYQQLLSFEESPQGRVLQIIVWGDYGRMDHKSFWGYAQILLDELEL 1546 : :			035168 PRELIMINARY; PRT; 1553 AA. 035168; 01-JAN-1998 (Trembrel) OS, Created)		Eukaryota; Medazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus. [1]	SEQUENCE FROM N.A. TISSUB-Brain; WEDLINE-37994473; PubMed=9252191; Wang V Oremote M schuite P Defense V Oremote M schuite P	"Rim is a putative Rab3 effector in regulating synaptic-vesicle fusion."; abutue 388:593-598(1997).	SIMILARITY: CONTAINS 1 PDZ/DHR DOWAIN. 1. ARO07836; AAB66703.1; 2. PZ10777; IRSY.	InterPro; IPR000008; C2. InterPro; IPR001360; Glyco_hydro_1. InterPro; IPR001478; PD2. InterPro; IPR001315; RPH3A effector	InterPro; IPR000306; Znf_FTVE. Pfam; PF00168; C2; 2. Pfam; PF00595; PDZ; 1. Pfam; PF00318; RPH3A effector: 1.	SMART; SM00239; C2; Z. SWART; SM00228; PDZ; 1. PROSITE; PS00152; ATPAS ALPHA BETA; 1. PROSITE; PS50004; C2 DOMAIN 2: 2.	PS00572; GLTCOSYL_HYDROL_F1_1; 1. PS50106; PDZ; 1. PS50178; ZF_FYVE; 1. 1553 AA; 172964 MM; D6643997E65D03EB CRC64;	54.2%; Score 4489.5; DB 11; Length 1553; Similarity 57.2%; Pred. No. 7.2e-273; 2; Conservative 209; Mismatches 319; Indels 183; Gaps 37;	SAPLGERGRPATPAASQPPPQPEMPDLSHLTEERKIILAVMDRQKKEERKGQSVLKI 60 :	110	LESNK 169

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--DYRHNGRDLQSSTLSVPRQVMSSNHCSPSGSPHRVDVIGRTRSWSPSAPPPQRNVEQG 1052
                                                                                                                                    61 KERHKAOPTOWFPFSGITELVNNVLOPOOKOPNEKEPOTKLHOOFENTKROVKONGEESO 120
                                                                                                                                                                    57 VVRDWAKDAA------CKTPRNAENQPHQPSPRLHQQPESYKEQVRKIGEEAR 103
                                                                                                                                                                                                                                           175
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  278 SEQNGYGALKSERKR.----VPKTSAQPVBGAVERERKER.-----RESRRL 319
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                575 SESVSEKGDSQKGKRKTSEQGVLSDSNTRSERQKKRMYYGGHSLEEDLEWSEPQIKDSGV 634
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                612 GRMTDLGRLGAFITKVKKGSLADVVGHLRAGDBVLEMWGKPLPGATNEBYNIILESKSE 671
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    POVELVVSRPIGDIPRIPDSTHAQLESSSSSFESQIONDRPSISVTSPMSPGMLRDVPQFL 814
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                                         msaplgprgrpappppaasopppppppmpdlshljtberktitlavmdrokkerkegsvlkt
                                                                    QQQ-BQKGDAPTCGICHKTKFADGCGHNCSYCQTKPCARCGGRVSLRSNK----VMWVCN
                                                                                                                                                                                                                                                                                                                            176 LCRKQQBILITKSGAMFYNSGSNTLQQPDQKVPRGLRNE-----RAPQEKKAKLHEQPQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           320 EKGESGDY---PDTPEKKDEGKAADEEKQRKEEDYQTRYRSDPWLARYPVKPPPEGQMR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      515 ETMLRNDSLSSDQSESVRPPPPRPHKSKKGGKMRQVSLSSSEERLASTPRYTSCDDVELE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           635 DTCSSTTLNEEHSBEKHPVTWQPSKDGDRLIGRILLINKRLKDGSVPRDSGANLGLKVVG
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921; Conservative 203; Mismatches 303; Indels 206; Gaps
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                                                                                                                               GSQSDTAVGALGTSGKKRRSSIGAKMVAIVGLSRKSRSASQLSQTEGGGKKLRSTVQRST 1367
                                                                                                                                                                                                                                                                                                                          1332 BTGWAARMRK-MVROPSRESTDGSINSYSSEGNLIFPGVRVGPDSQFSDFLDGLGPAQLV 1390
                                                                                                                                                                                                                                                                                                                                                                                            GROTLATPAMGDIQVGMDKKGQLEVBIIRARGLVVKPGSKTLPAPYVKVYLLDNGVCIA 1487
                                                                                                                                                                                                                                                                                                                                                                                                                     KKKTKVARKTLEPLYQQLLSFEESPQGRVLQIIVMGDYGRMDHKSFMGVAQILLDELELS 1547
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ETGLAVEMENNMIRQASRESTDGSMNSYSSEGNLIFPGVRLASDGPEDGLGPAQLV
              M--KLNKYKQV--AGSDPRLEQDYHSKYRSGWDPHRGADTVSTKSSDSDVSDVSAVSRTS
                                                                                                       SASRESSTRYMSVOSERPRGNRKISVFTSKMQNRQMGVSGKNLTKSTSISGDMCSLEKND
                                                                                                                                                                                                                             Morohashi A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606,
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A RACYAM M.A.

A RACYAM M.A.

A RACY T., Nakagawara A.;

"Identification of the alternative form of human RIM.";

"Interpro; IPRO0008; C2.

"Interpro; IPRO00345; Cytc. heme bind.

"Interpro; IPRO01345; Cytc. heme bind.

"Interpro; IPRO01345; Cytc. hydro...

"Interpro; IPRO01345; Cytc. hydro...

"Interpro; IPRO03315; RPH3A effector.

"Interpro; IPRO03315; RPH3A effector.

"Interpro; IPRO03045; Cytc. TYVV.

"Interpro; IPRO03045; Cytc. TYVV.

"Interpro; IPRO03045; Cytc. TYV.

"Interpro; IPRO03045; Cytc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SWIGWYKLPPPSSLVDPTLAPLTRRASQSSLRSSSGPPCIRS 1553
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PSS0178; ZF FYVE; 1.
1470 AA; 164001 MW; 63FD24F44A6E739A CRC64;
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Last sequence update)
Last annotation update)
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SWART; SM00239; C2; 2.
SMART; SM00228; PDZ; 1.
PROSITE; PS50004; C2 DOMAIN 2; 2.
PROSITE; PS00199; CTTOCHROME C; 1.
PROSITE; PS00199; CTTOCHROME C; 1.
PROSITE; PS00172; GLYCOSTL HTDROL_F1 1; 1.
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01-JUN-2002 (TrEMBLrel. 21,
01-MAR-2003 (TrEMBLrel. 23,
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Best Local Similarity
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NBLA00761.
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SEQUENCE
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Q8TDY9
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SOR BREAK BR

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104 RYQGEHXDDAPTCGICHKTKFADGCGHLCSYCRTWFCARCGGRVSLRSNNEDKVVWWVCN 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    176 LCRKQQBILITKSGAMFYNSGSNTLQQPDQKVPRGLRNG-----EAPQEKKAKLHEQPQ 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          229 FQ-----GAPGDLSVPAVEKGRAHGL--TRQDTIKGSGGVKHQIASDMPSDRKRSPSV 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   218 SQTPLSTAAASSQDAAPPSAPPDRSKGABPSQQALGPRQKQASSRSKSKSEBPRERKKTPGL 277
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         278 SBQWGKGALKSERKR-----VPKTSAQPVBGAVEBREKKER-------RESRRL 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 340 CHRHSKRYIVDDEDVESRDE----YERQRREEEYQARYRSDPWLARYPVKPQPYEEQMR 394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        320 EKGRSQDY----PDTPEKRDEGKAADSEKQRKEEDYQTRYRSDPNLARYPVKPPPEEQQMR 376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    395 IHAEVSRARHERRHSDVSLANAELEDSRISLLRMDRPSRQKSVSERRAAMENQRSYSMER 454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TRRACCOSSYPORTSNHSPPTPRRSPIPLDRPDMRRADSLRKCHHLDPSSAVRKTKREKM 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       483 -LMLRNDSLSSDQSESVRPSPPKPHRSKRGGKRRQMSVSSSSBEBGVSTPRYTSCEDVELE 541
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               164 LCRKQQBILITKSGAMFFGSG------PQQTSQDGTLSDTATGAGSEVPREKKARLQERSR
                                                                                                                                                                                                                                                                                   121 QQQ-EQKGDAPTCGICHKTKFADGCGHNCSYCQTKPCARCGGRVBLRSNK----VMNVCN
                                                                                                                                                                                                                                                          1 MSAPLGPRGRPAPTPAASQPPPQPEMPDLSHLTERERKIJILAVMDRQKKEREKEGSVLKI
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                                                                                                                                                                                                                    145;
                                                                                                                                                                      DB 4; Length 1028;
                                                                                                                                                                    Query Match 35.4%; Score 2936.5; DB 4; Length Best Local Similarity 54.1%; Pred. No. 1.2e-175; Matches 614; Conservative 143; Mismatches 232; Indels
                  SMART; SM00228; PDZ; 1.

PROSITE; PS50004; C2 DOMAIN 2; 1.

PROSITE; PS00190; CYTOCHROWE_C; 1.

PROSITE; PS50106; PDZ; 1.

PROSITE; PS50109; ZF FYVE; 1.

SRQUENCE 1028 AA; 115346 MW; 20BDCD96CA109D0F CRC64;
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                                                                                                                                           OPFLDRARSASTNCLRPDISL------HSPERERMHRQRSPTQSPPADISFS
                                                                                                                                                                                      1163 GRRGROLPQLPPK-GTLERSAMDIEERNROMKL--NKYKOV--AGSDPRLEQDYHSKYRS
                                                                                                                                                                                                                                                                            GWDPHRGADTVSTKSSDSDVSDVSAVSRTSSASRPSSTSYMSVQSERPRGNRKISVPTSK
                                                                                                                                                                                                                                                                                                   1195 MQGRRMGTSGRSIMKSTSVSGEMYTLEHNDGSQSDTAVGTVGAGGKKRRSSLSAKVVALV
                                                                                                                                                                                                                                                                                                                                                                                                                                                   GLSRKSRSASQLSQTBGGGKKLRSTVQRSTETGLAVEMENWMTRQASRESTDGSMNSYSS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             H--RGTRATGHYNTISRM---DRHRVMDDHYSSDRDRDCEAADRQPYHRS-----RSTEQ
                                                                                                   RPLLERTTTRSRSSERPDTNLMRSMPSLMTGRSAPPSPALSRSHPRTGSVQTSPSSTPGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1458 ARGLVVKPGSKTLPAPYVKVYLLDNGVCIAKKKTKVARKTLBPLYQQLLSFERSPQGRVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1518 QIIVWGDYGRMDHKSFWGVAQILLDELELSNWVIGWFKLFPPSSLVDPTSAPLTRRASQS
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Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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Last sequence update)
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InterPro; IPR000345; Cytc heme bind.
InterPro; IPR001478; PDZ.
InterPro; IPR001315; RPH3A effector.
InterPro; IPR00306; Znf FTVE.
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Pfam; PF00595; PDZ; 1.
Pfam; PF02318; RPH3A_effector; 1.
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01-JUN-2002 (TrEMBLrel. 21,
01-MAR-2003 (TrEMBLrel. 23,
RIM short form.
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Db 792 KILEPKWNQTFVYSHVHRRDFREMLEITVWDQPRVQEBRSEFLGEILIELETALLIDDEP 851

Qy 935 HWYKLQTHDVSSLPLPRPSPTLPRRQLHGRSPTRRLQRSKRISDSEVSDYDCEDCWGVVS 994

B52 HWYKLQTHDVSSLPLPRPSPTLPRRQLHGRSPTRRLQRSKRISDSEVSDYDCEDCWGVVS 994

Cy 995 --DYRHNGRDLQSSTLSVPEQVMSSNHCSPSGSPHRVDVIGRTRSWBPSAPPPQRAVEGG 1052

Db 912 PVGYRSSARESKSTTLTVPEQORTTHHRSRSVSPHRGNDQGKPRSRLPNV-PLQRSLDEI 970

QY 1053 H--RGTRATGHYNTISRM---DRHRVMDDHYSSDRDECRAADRQPYHRSRSTE 1101

Db 971 HPTRRSRSPTRHHDASRSPVDHRTRDVDSQYLSEQDSELLMLPRA--KRGRSAE 1022

Search completed: December 12, 2003, 07:16:36

Job time: 99 secs
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

December 11, 2003, 23:16:12 ; Search time 40 Seconds (without alignments) 1869.312 Million cell updates/sec Run on:

Title: Perfect score: Sequence:

US-09-617-099B-1 8285 1 MSAPLGPRGRPAPTPAASQP.....TRRASQSSLESSTGPSYSRS 1590

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

127863 seqs, 47026705 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

1,

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_41:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	•	Description	O9Du36 callus call	homo		_		-		mus m	P47709 rattus norv		home	Q9jix8 mus musculu	P12270 homo sapien		-		Domod	pollo	THE STATE	pour	homo	rattu	P49750 homo sapien	ovis	Q61687 mus musculu	oryc		ELLE.	Caen		pomor	212
SUMMAKIES	;	αī	PCLO CHICK	PCLO HUMAN	PCLO_RAT	PCLO_MOUSE	YPT7 CAREL	TRHY HUMAN	RP3A HUMAN	RP3A MOUSE	RP3A RAT	RP3A BOVIN	APC HUMAN	ACIN MOUSE	TPR HUMAN	APC RAT	APC_MOUSE	MAPB HUMAN	ACIN HUMAN	NCR1 HUMAN	NKCR MOUSE	NKCR HUMAN	MAPA HUMAN	MAP2 RAT	ZAP3_HUMAN	TRHY SHEEP	ATRX MOUSE	TRHY RABIT	TP20 MOUSE	NCR1 MOUSE	ATRX CAERL	ANK3 HUMAN	BAT2 HUMAN	MAD2 MOTISE
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*		March	7.7	6.7	6.7	9.9	4.1	3.7	3.5		3.5	3.5	3.1	3.1	3.1	3.1	3.1	3.1	3.1	3.1	3.0	5.9	2.9	2.9	6.9	5.3	2.9	•	•	2.8	•	•	2.7	2.7
		Score	637	555.5	555	545.5	338	307	267.5	264	262.5	261.5	258.5	258	255.5	255	254.5	254	253.5	253	248.5	244	244	242	241.5	241	239.5	233.5	232	230.5	225	224.5	223	221.5
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ZOZ HUMAN PADJ MOUSE AACJ HUMAN MAPA RAT MAPB RAT ILVA DROME PADJ RAT UN13 CAREL TOOP HUMAN ZOZ CANFA
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ALIGNMENTS

RESULT 1

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ដ	(Rel. 41, Last
Ė.	28-FEB-2003 (Rel. 41, Last annotation update)
ឌ	ein (Aczonin) (
3 8	PCLO OR ACZ.
38	Control gatter (Chickell)
3 8	Archigantis Base Macmathan Callifornia Vertebrates Buteleostomi;
8	Allosaulia, Aves; Necomaliae; Gailliolmes; Phasianidae; Phasianinae; Gallus.
ğ	NCBI TaxID=9031;
Ş	_ [1]
RP.	SEQUENCE PROM N.A.
ည္က	TISSUR=Brain;
×	MEDLINE=99439764; PubMed=10508862;
2 2	Wang K., Kibschull M., Laue M.M., Lichte B., Petrasch-Parwez E.,
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¥ 6	550-Kd putative scattolding
† £	Action, minister monitory regions with rim and bassoon and binds
12	J. Cell Hill 147.15.152/1000)
일	CONTRACTOR THAT ILLY FOR FINANCIAL ASSESSMENT ASSESSMEN
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ខ	trafficking (By similarity)
ខ	-!- SUBUNIT: Interacts with Pahaci/Drai and profiling for similarians
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ខ	3
ខ	-1- DOMAIN: C2 domain 1 is involved in binding calcium and
ខ	phospholipids. Calcium binds with low affinity but with high
ខ្ល	specificity and induces a large conformational change.
ပ္ပ	
ខ្ល	SIMILARITY
ខ្ល	
ខ	This SWISS-PROT entry is copyright. It is produced through a collaboration
38	Detween the Swiss Institute of Bioinformatics and the EMBL outstation -
38	the Kuropean Bioinformatics Institute. There are no restrictions on its
36	use by non-profit institutions as long as its content is in no way
ខ	motive and the process arresponding to the confidence of the confi
ខ	or send an email to licensee is a licensee is the management of substitution of send an email to licensee is a licensee is the control of the
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ă	Y19187; CAB60725.1;
D.R.	HSSP; P04410; 1A25.
ř	
ž	GO; GO:0005509; F:calcium ion binding activity; 188.
ន	GO; GO:0005544; F:calcium-dependent phospholipid binding acti ; ISS.
8 8	•
ž	GO; CO: 0001010; P:cytoskeleton organization and biogenesis; 188.
ž 2	GO; GO:0016080; P:8ynaptic vesicle targeting; ISS. Interpro. Ibbonoons. C.
ន័ក	ALCETIC) IFKNOUNUS CZ. Interpro. IDBA01478. Dh7
ä	IPR001565;
S.	0168; C2; 2

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1108 RITIRSRSSERPDINIARSMPSLATGRSAPSPALSRSHPRIGGSVQISPSSTPGTGRRGR 1167
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1495 QQCGRARICVRLDIAMILSDSENPQHIEIHRÞVKAVDKAKSPGVDÞKQLAÀRIQKVSIQQA 4554
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                                                                                                                                                                                                                                                                                                                    4675 RIKXVQXSLNPENNQTVIXKNISTEQLXXXTLEVTVMDTDRF--SSNDFLGEVLIDLSSV 4732
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                                                                                                                                                                                              VVGGKMT--ESGRLCAFITKVKKGSLADTVGHLRPGDEVLENNGRLLAGGATFEEVYNIIL 749
                                                                                                                                                                                                                                       LSIKLWFDKVGHQLIVTILGAKDLPSREDGRPRNPYVKIYFLPDR-----SDKNKR 868
                                                                                                                                                                                                                                                                                                  RIKIVKKILEPKHNOTFIYSPVHRREFRERMIRITLANDARVRERESEFLGRILIELET- 927
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                                                                                                               750 KSKPRPOV------ELVVSRPIGDIPRI-----PDSTHAQLE----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1048 NVEÇGHRGTRATGHYNTISRMDRHRVMDDHYSSDRDRDCEAADRQPYHRSRSTEGRPLLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KSHSSPGSKSSSBGHLRS-----HGP-----SRSQSKTSVTQT-----
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PCIO HUMAN STANDARD; PRT; 5147 AA.
ID PCIO HUMAN STANDARD; PRT; 5147 AA.
AC Q9Y6\(\vec{V}\)043373; 066305; Q9BVC8; Q9UIV2; Q9Y6U9;
DT 28-FEB-2003 (Rel. 41, Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -POHLINYRDSINRRGHRHSKEYIVDDEDVESRDEYERQRREEEYQARYRSDPINLARYPVKP 386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ----VKRWGEB------SQQQQEQKGDAPTCGICHKTKFADGCGHNCSYCQTKFCARC 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            218 EKKAKLHEQPQPQGAPGDLSVPAVEKGRAHGLTRQD------TIKNGSGVKHQIASDM 269
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                                                                                                                                                                                                                                                                                                                                                                                                                                     KHKAQPIQWPPFSGITELVNNVLQPQQKQ-PNEKBPQTKLHQQPEMYKBQ------
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P-A-K-P-Q-P-Q-Y-C-Q-Y-R
C4-TYPE (POTENTIAL).
C4-TYPE (POTENTIAL).
Pfam; PF00595; PDZ; 1.
PRINTE; PR00399; SYNAPTCTAGAN.
SMART; SM00229; CZ; 2.
SMART; SM00229; CZ; 2.
SMART; SM00229; CZ DOMAIN 1; 1.
PROSITE; PS00499; CZ DOMAIN 2; 2.
PROSITE; PS50106; PDZ; 1.
Calcium/phospholipid-binding; Zinc; Metal-binding; Zinc-finger;
                                                                                                                                                                                                                                                                                                                              Best Local Similarity 21.2%; Pred. No. 2.8e-22;
Matches 367; Conservative 226; Mismatches 556; Indels 582;
                                                                                                                                                                                                                                                                                                               7.7%; Score 637; DB 1; Length 5120; 21.2%; Pred. No. 2.8e-22;
                                                                                                                                                                                                                                                                                  MW; A658D9891B65B412 CRC64;
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POLY-PRO.
PDZ.
C2 DOMAIN 1.
C2 DOMAIN 2.
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2324 2343
4414 4493
4627 4726
5003 5094
5120 AA; 560751 M
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A MEDINE-22388257; PubMed-12477932;

A Krausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

A Klausner R.D., Collins F.S., Wagner L., Shemen C.M., Schuler G.D.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Raha S.S., McKwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gabbs R.A.,

RA Hichards S., Worley K.C., Hale S., Garcia A.M., Gabbs R.A.,

RA Hichards S., Worley K.C., Hale S., Garcia A.M., Gabbs R.A.,

RA Hichards S., Worley K.C., Shevchenko Y., Bouffard G.G.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Ruterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

RA Schnerch A., Scheln J.S., Jones S.J.M., Marra M.A.;

Ruterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

RA Homan and mouse cDNA sequences.";

R Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                  "Aczonin, a 550-kd putative scaffolding protein of presynaptic active zones, shares homology regions with rim and bassoon and binds profilin.",
                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 3619-5147 FROM N.A. (ISOFORM 2).
TISCUSTBEATH,
MEDLINE=98290545; PubMed=9628581;
Nagase T., ISALKawa K.-I., Miyajima N., Tanaka A., Kotani H.,
Nomura N., Chara O.;
Nomura N., Chara O.;
The complete sequences of unidentified human genes. IX.
The complete sequences of 100 new CDNA clones from brain which can
code for large proteins in vitro.";
                                                                                                 Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
NCBI TaxID=9606;
                                                                                                                                                                                                                  MEDLINE-99439764; PubMed-10508862;
Wang X., Kibachull M., Laue M.M., Lichte B., Petrasch-Parwez B.,
Kilimann M.W.;
                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 552-4404 FROM N.A.
Kraemer J., Wollam C., Wohldmann P., McGrane B.;
Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
28-FEB-2003 (Rel. 41, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Piccolo protein (Aczonin) (Fragments).
PCLO OR ACZ OR KIAA0559.
Homo saplens (Hunan).
                                                                                                                                                                                                                                                                                                                                            Cell Biol. 147:151-162(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 4405-4439 FROM N.A.
                                                                                                                                                                             SEQUENCE OF 1-759 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA Res. 5:31-39(1998).
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Kalloki J., Elliott G.;
Kalloki J., Elliott G.;
Submitted (FEB-1998) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: May act as a scaffolding protein involved in the organization of synaptic active zones and in synaptic vesicle trafficking (By similarity).
-!- SUBUNIT: Interacts with Rabacl/Fral and profilin (By similarity).
-!- SUBCELLUAR LOCATION: Concentrated at the presynaptic side of synaptic junctions (By similarity).
-!- ALTERNATIVE PRODUCTS:

IsoId=Q9Y6V0-2; Sequence=VSP_003923, VSP_003924, VSP_003925, lsold=Q9Y6V0-1; Sequence=Displayed; Name=2; Name=1

Bvent=Alternative splicing; Named isoforms=2; Comment=Additional isoforms seem to exist;

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C2 DOMAIN 2.
S -> SACHLIGHTUNGKEIPCHSGEIGAYIAKILPGGSAE GYGHLGHTUNGKEIPCHSGEIGAYIAKILPGGSAE GYGHLAWEG (in isoform 2).
/FTIG=VSP 003923.
/FTIG=VSP 003924.
G -> GQYMVVQRAS (in isoform 2).
/FTIG=VSP 003925.
TAHKS -> ŠKRKK (in isoform 2).
/FTIG=VSP 003926.
Missing (in isoform 2).
/FTIG=VSP 003926.
Missing (in isoform 2).
/FTIG=VSP 003926. 316 RRSQREPQFYEEPGHLNYRDSNRRGHRHSKEYIVDDEDVESRDEYR----RQRREEEYQ- 370 GO; GO:0005856; C:cytoskeleton; MAS.
GO; GO:0005809; C:cytoskeleton; ISS.
GO; GO:0005509; F:calcium ion binding activity; ISS.
GO; GO:0005544; F:calcium-dependent phospholiphi binding acti. .; ISS.
GO; GO:0005524; F:calcium-dependent phospholiphi binding acti. .; ISS.
GO; GO:0007010; P:cytoskeleton organization and biogenesis; ISS.
GO; GO:0007010; P:synaptic vesicle targeting; ISS. 10 x 10 aa tandem approximate repeats of P-a-K-P-Q-P-Q-Q-P-X. C4-TYPE (POTENTIAL). C4-TYPE (POTENTIAL). Query Match 6.7%; Score 535.5; DB 1; Length 5147; Best Local Similarity 21.8%; Pred. No. 2.1e-18; Matches 308; Conservative 208; Mismatches 488; Indels 407; Gaps Note=No experimental confirmation available, DOWAIN: C2 domain 1 is involved in binding calcium and phospholipide. Calcium binds with low affinity but with high specificity and induces a large conformational change. SIMILARITY: Contains 2 C2 domains. SIMILARITY: Contains 1 PDZ/DHR domain. InterPro; IPR0000009; C2.
InterPro; IPR001565; Synaptotagmin.
PRINTS; PR00360; C2DOMAIN.
PRINTS; PR00360; C2DOMAIN.
PRINTS; PR00499; C2_DOMAIN.1; 1.
PROSITE; P800499; C2_DOMAIN.1; 1.
PROSITE; P8500499; C2_DOMAIN.2; 2.
Calcium/phospholipid-binding; Zinc; Metal-binding; Zinc-finger;
NON_TER. 5147 AA; 563537 MW; CD5D84990498CD3C CRC64; VSP_003926, VSP_003927; POLY-PRO. EMBL; AC004903; AAD2036.1; -EMBL; AC004806; AAD21789.1; -EMBL; BC011311; BAA25485.1; -EMBL; BC001304; AAH01304.1; -EMBL; AC004082; AAB97937.1; -EMBL; AC064082; AAB97937.1; -EMBL; AC06410.1 AAS.
Genew; HGNC:13406; PCLO.
MIM; 604918; --EMBL; Y19188; CAB60727.1; -. 1011 2325 4442 4633 5121 4404 4761 5147 4534 4576 4576 4757 4762 4534 400 ZN FING PARSPLIC VARSPLIC VARSPLIC VARSPLIC SEQUENCE PARSPLIC Query Match DOMAIN DOMAIN DOMAIN DOMAIN DOMAIN ò ద

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371ARXRSDPMLARYPVKPQPYEEQMRIHAEVSRARHERR 407	HSDVSLAN-AELEDSRISLIANDRPSRORSVSERRAAMENGRSYSMERT	4090 LIDPKMSKFSPIQESKDLEPDYSSYMTSSTSSIGGISSRARLLQDDITFGLRKNITDQ 4147		QKFMGSSLGTGLGTLGNT1RSALQDRADKPYSSGSRSRPSSRPSSVYGLDL\$1	495 RKQHHLDP8ARVRITKREMBTHLRNDSLASDQSBSVRPPPRFHKSKKGKRRRRLSS 554 4201 KRDSSSSSLRLKAQEARALDVSPSHASBSARTKPTSLPISQSRGRIPIVAQNS 4253	555 SERELASTPEYTSCDDVELESESVSEKGDSQKGKRKTSRQGVLSDSNTRSERQKKRMYG 614	4254 BEBSPLSPVGQPWGWARAAAGPLPPISADTRDQFGS 4289	615 GHSLEEDLEWSEPQIKDSGVDTCSSTTLNE-EHSHSDKHPVTWQPSKDGDRLI 666	SHSLPEVQQIMREESRTRGYDRDIAFINDDPQHAMSDSEAYHLRREETDWFDKPRESRLE	667 GRILLINKELKDGSVPRDSGAMLGIKVVGGRWTESGRLCAPITKVKKGSLADTVGH 721 :: ::	LRPGDEVLEWNGRLLQGATFEEVYNIILESKPEPOVELVVSRPIGDIPRIPDSTHAOLES	QVLEWNGIPLISKTYEKVQSIISQQSGRABICVRLDLAMLSDSENSQHLELHE	782 SSSSFBSQKMDRPSISYTSPM 802	4459 PPKÄVDKAKSPGVDPKQLAAELQKVSLQQSPLVLSSVVEKGSHVHSGPTSAGSSGVPSPG 4518	03	4519 QPG8-PSVBKKKHGSSKLQINYÖ-LGN-LIIHILQARNLVPRDNNGYSDPRVKYTLLPGR 4575	863 SDKNKRRIKTVKKTLEPKNNQTFIYSPVHRREFRERMLEITLMDQARVREBSBFLGEIL 922	٦ ١	IDLSSTBHLONTPRWYPLKRQTESIDHGKSHSSQSSQQSPKPS-	979 SEVSDYDCEDGVGVVSDYRHNGRDLQSSTLSVPRQVMSSNHCSPSGSPHRVDVIGRTRSW 1038	4677VIKSRSHGIFPDPSKDMQVPTIEKSHSSFGSSKSSEE-GHLRSH 4719	1039 SPSAPPPQRNVEÇGHRGTRATGHYNTISRMDRHYSUNDDHYSSDRDCRAADRQPYHRSR 1098	4720 GPSRSQSKTSVTQTH 4751	STEORPLIERTTTRSRSSERPDTNIARSMPSL-MTGRSAPPSPALSRSHPRTGSVQTSPS : : : : : : : : :	NHARKQHRHSIAG	STPGTGERGRQLPQLPPRGTLERSAMDIBERNRQMKLNKYKQVAGSDPRLBQDYHSKYRS	VLPIGRTGSDNLPP-PANGNGDGSQLALRYVMSDGPVKP	1218 GWDFHREAD-TVSTKSSDSDVSDVSAVSRTSSASRFSSTSYMSVQSERFRGNRKISVF 1274	TORMUNDOMETRICATION OF THE PARTY OF THE PART		1329 -IGAKMVAIVGLSRKSRSASQLSQTBGGGKKLRSTVQRSTETGLAVEMRNWM 1379
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                                                                                                    PAMGDIGVGM---MDKKG-QLKVEIIRARGLVVKPGSKT-LPAPYVKV 1477
                                                                                                                                                                                                                                                   CKTKVARKTLEPLYQQLLSFEESPQGRVLQIIVWGDYGRMDHKSFMG 1535
                                                                      WNSYSSEGNL-IFPGV---RLASDSQF-----SDFLDGLG 1422
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with Rabaci/Frai and profilin.

Noncentrated at presynaptic side of synaptic
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hordata; Craniata; Vertebrata; Buteleostomi;
odentia; Sciurognathi; Muridae; Murinae; Rattus.
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Med=10707984;
.J., Zhai R., Cases-Langhoff C., Voss B.,
K. Mindler S., Gundelfinger R.D., Garner C.C.,
ic zinc finger protein structurally related to
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., Rizo J., Suedhof T.C.;
in in the active-zone protein piccolo:
+) tegulation of neurotransmitter release.";
2001).
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anghoff C., Gundelfinger B.D., Garner C.C.;
to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IITY, AND MUTAGENESIS OF ASP-4668; ASP-4674;
AL-4690; BER-4691; GLN-4692; ASN-4693 AND
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Last sequence update)
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(domain presynaptic cytomatrix protein).
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or send an email to licenseélsb-sib.ch).
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VV->SS: 10-FOLD INCREASE IN APPINITY FOR
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6.7%; Score 555; DB 1; Length 5085;
Best Local Similarity 20.8%; Pred. No. 2.2e-18;
Matches 298; Conservative 191; Mismatches 380; Indels 564; Gaps
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AND CALCIUM-DEPENDENT PHOSPHOLIPID
BINDING ACTIVITY.
                                                                                                                                                                                                                                                                                                                                                                                                     /FILS-VSP 003931.
D->A: COMPLETE LOSS OF CALCIUM-BINDING
AND CALCIUM-DEPENDENT PHOSPHOLIPID
                                                                                                                                                                                                                                                                                     12 X 10 AA TANDEM APPROXIMATE REPEATS P-A-K-P-Q-P-X. C4-TYPE (POTENTIAL). C4-TYPE (POTENTIAL).
                                                                                                      GO:0045202; C:synaptic junction, IDA.
GO:0045202; F:calcium ion binding activity; IDA.
GO:0005544; F:calcium-dependent phospholipid binding acti..
GO:0005522; F:profilm binding activity; ISS.
GO:0007010; P:cytoskeleton organization and biogenesis; ISS.
GO:0016080; P:synaptic vesicle targeting; NAS.
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InterPro; IRR00008; C2.
InterPro; IRR001478; PDZ.
Ffam; PF00168; C2; 2.
SWART; SW00239; C2; 2.
SWART; SW00239; C2; 2.
SWART; SW00249; C2 DOMAIN 1; 1.
PROSITE; PS50004; C2 DOMAIN 2; 2.
PROSITE; PS50016; PDZ; 1.
Calcium/phospholipid-binding; Metal-binding; Zinc; Zinc-finger;
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C2 DOMAIN 1.
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TKPIN -> SKRK (in isoform
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Missing (In isoform 2).
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                                                                         EMBL; AF138789; AAF07822.2; -. EMBL; AF227534; AAF63196.1; -.
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4639 983 DYDCEDGVGVVSDYRHNGRDLQSSTLSVPEQVMSSNHCSPSGSPHRVDVIGRIRSMSPSA 1042 GRRGRQLPQLPPKGTLKRSAMDI --- BERNROMKLNKTKGVAGSDPRLEQDYHSKYRSGW 1219 QNRQMGVSGRNLIKSTSISGDMCSLKKNDGSQSDTAVGALGTSGKK--KRSSIGAKNVAL 1336 VGLSRKSRSASQLSQTEGGGKKLRSTVQRSTETGLAVENENMITRQAGRESTDGSMNSYS 1396 -----TDTEG-----KTQVMGEIKLALKKEMK------TDGE----- 4967 926 -ETALLDDEPHWYKL--QTHDVSSLPLPRPSPYLPRRQLHGRSPTRRLQRSKRISDSEVS 982 1365 AFINDDPOHAMSDSBAYHLRREETDWFDKPRESRLENGHGLDRKLPERLVHSRPLSOHOB -----BEQGVISDSNTRSEROKKRMYY------CGHSLE----EDLEWSEPQIK-DS 633 GVDTCSSTTLNEEHSHSDKHPVTWQPSKDGDRLIGRILLNKRLKDGSVPRDSGAMLGLKV 1425 OILOMNGKTIHYIPPHA----------RVKITRDFKDHT---GSGNGLGIRI VOGROUT -- ESGRICAFITKVKKGSLADTVGHLRPGDBVLKNNGRLLQGATFEEVYNIILE 4464 VGGKRIPGHSGRIGAYIAKILPGRSARHTGFLAMGAQVLBWGVPLTSKTYBEVQSIINQ 1580 QSPLVMSSVVEKGSHAHSGPTSAGSSSVPSPGQPGSPSVSKKKHSSTKPTDGPKAASHPI SGQLSIKLWFDKVGHQLIVTILGAKDLPSREDGRPRNPYVKIYFLPDR-----SDK 866 NKRRIKTVKKTLEPKNNQTFITSPVHRREFRERMLEITLNDQARVREERSEFLGEILIEL 1043 PPPQRNVEQGHRGTRATGHYNTISRMDRHRVMDDHYSSDRDRDCBAADRQPYHRSRSTBQ *305 BÄRSPLSPVGQPMGMARAAAGPLPPISADTRDQPGSSHBLPRVQQHMREKSKIRGYDRDI 751 SKPRPQV------PDSTHAQLESSS--4698 YERRIKYVQKSIAPEWNQTVIYKSISMEQIAMKKTLEVTVWDYDRF--SSNDFLGEVLIDL RKQHHLDPSSAVRKTKREKMETMLRNDSLSSDQSRBVRPPPRPHKBKKGGKMRQVSLSS 1103 RPLLERTTTRSRSSERPDTNLMRSMPSLMTGRSAPPSPALGRSHPRTGSVQTSPSSTPGT 1220 DPHRGAD-TVSTKSSDSDVSDVSAVSRTSSASRRSSTNSVQSKRPRGNRKISVFTSKM 1880 - WHRPAESSYSTCSSGSSYG------SGTSYDSE-----4756 SSTSHLDNTPRWYPLKEGIRSID------HGKS---------HSSQNSQQS--PKPSVIKSRSH-----SEERLAS-------TPEYTSCDDVELESESVSEKGDSQKGKEKT

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SEGNLIFPGVRLASDSQFSDFLDGLGPAQLVGRQTLATPAMGDIQVGMADKKGQLEVEII 1456
                                         1457 RARGLVVKPGSKT-LPAPYVKVYLLDNGV--CIAKKKTKVARKTLEPLYQQLLSFEBSPQ 1513
                       4968 ------QLIVEIL 4974
                                                                                                                                                                                                                                                                                                                                                                 "Aczonin, a 550-kd putative scaffolding protein of presynaptic active zones, shares homology regions with rim and bassoon and binds profilin.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Isold=090XX7-2; Sequence=VSP_003928, VSP_003929; TISSUE SPECIFICITY: Highly expressed in brain. Low levels found in stomach. Not detected in other tissues analyzed including adrenal.
                                                                                     1514 GRVLQIIVWGDYGRMDHKSFMGVAQILLDELELSNMVIGWFKLPPPSSLVDPT 1566
                                                                                                  (Aczonin) (Brain-
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Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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Wang X., Kibschull M., Laue M.M., Lichte B., Petrasch-Parwez B.,
Kilimann M.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     trafficking.
-!- SUBCELLULAR LOCATION: Concentrated at the presynaptic side.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Huang W., Jin W., Huang C., Chen B., Zhang J., Ju G.;
Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: May act as a scaffolding protein involved in the
                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A., SUBCELLULAR LOCATION, ALTERNATIVE SPLICING.
TISSUE SPECIFICITY, AND INTERACTION WITH PROFILIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                         090YX7; 090YX6; 090ZJ0;
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Piccolo protein (Presynaptic cytomatrix protein)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                5038 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IsoId=09QYX7-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                               Cell Biol. 147:151-162(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 4502-4682 FROM N.A. TISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -1- ALTERNATIVE PRODUCTS:
                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                        Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                       NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                    TISSUE=Brain;
                                                                                                                                                                                                                                           PCLO OR ACZ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kilimann M.;
                                                                                                                                                                 MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                    REVISIONS
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EMBL; Y19185; CA860731.2; -

DR EMBL; Y19185; CA860731.2; -

DR REAL; API81269; AAD55786.2; -

DR REAL; API81269; AAD55786.2; -

DR REAL; API81269; AAD55786.2; -

DR RESP; P04410; 1A25.

DR MGD; WAI:1349390; Pclo.

DR GO; GO:0005502; C:synaptic junction; IDA.

GO; GO:0005524; F:calcium-dependent phospholipid binding acti. .; ISS.

GO; GO:0005522; F:profilin binding activity; IDA.

GO; GO:0005522; F:profilin binding activity; IDA.

GO; GO:00007010; P:cytoskeleton organization and biogenesis; IDA.

GO; GO:0016800; P:synaptic vesicle targeting; NAS.

InterPro; IFR00108; C2.

InterPro; IFR001478; PDZ.

REAL; SMO0229; PDZ.

SMART; SM00229; C2; 2.

SMART; SM00229; C2; 2.

SMART; SM00229; C2; 2.

PROSITE; PSS0004; C2 DOWAIN 1; 1.

PROSITE; PSS0106; PDZ, 1.

RESPONDED: PDZ, 1.

REPOSITE; PSS0106; PDZ, 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4092
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3984 RRSQBVTDF-----LAPLQTSSRLH---SYVKAEED-PMEDPYELKLLKHQIKQEFRR 4032
commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1317 AFIMDDFQHAMSDSEAYHLRREETDWFDKPRESRLENGHGLDRKLPERLVHSRPLSQHQE 4376
                                   (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          456 ------PLDRPDMRRADSL 494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              633 GYDTCSSTTLNEEHSHSDKHPVTWQPSKDGDRLIGRILLANKRLKDGSVPRDSGAMLGLKV 692
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10 X 10 AA TANDEM APPROXIMATE REPEATS OF P-A-K-P-Q-P-X.
P-A-K-P-C-P-D-Q-P-X.
C4-TYPE (POTENTIAL).
C4-TYPE (POTENTIAL).
POLY-PRO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4033 GTESLDHLAGLSHYYHADTSYRHFPKSEKYSISRLTLEKQAAKQLPAAILYQKQSKHKKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1151 QKFMGSSLGSGLGTLGNTIRSALQDBADKPYSSGGRSRPSBRPSSVYGLDL----SI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               408 HSDVSLAN-AELEDSRISLLRMDRPSRQRS-----VSERRAAMENQRSYSMERT---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    495 RKOHHLDPSSAVRKTKREKMETMLRNDSLSSDOSRSVRPPPRRPHKSKKGGKMRQVSLSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ----SEQGVLSDSWTRSERQKKRMYY-----GGHSLR----EDLEWSEPQIK-DS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RRSQREPOFYEEPGHINYRDSNRRGHRHSKEYIVDDEDVESRDEYE----RQRREEFYQ-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ------ARYRSDPNLARYPVKPQPYEEQ--MRIHAEV---SRARHERR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          555 SEERLAG-----TPEYTSCDDVELESESVSEKCDSQKCKRT----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 6.6%; Score 545.5; DB 1; Length 5038; Best Local Similarity 20.6%; Pred. No. 6.2e-18; Matches 295; Conservative 192; Mismatches 384; Indels 561; Gaps
    and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C2 DOWAIN 1.
C2 DOWAIN 2.
TKPIN -> SKRRK (in 1soform 2)
FFIGH-VSP_003928.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4834 5038 Missing (In isoform 2).
/FTId=VSP 003929.
5038 Aa; 547600 MW; DADA460CF3B40888 CRC64;
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yota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea; litidae; Peloderinae; Caenorhabditís. TaxID=6239;

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ą	. : :: :: :	DT 01-NOV-1995 (Rel. 32, Last sequence update) DT 16-OCT-2001 (Rel. 40, Last annotation update)
è 8	693 VGGKWTBSGRLCARITKVKKGSLADTVGHLRPGDBVLEMNGRLLQGATFEBVYNIILE 750	
È		C. Aukaryota, Metazoa, Nemaroda, Chromadorea, Rhabditida, Rhab OC Rhabditidae, Peloderinae, Caenorhabditis. OX NCBI TaxID=6299
q	4476 QSGEARICVRLDIAMLSDSEXPQHLEIHBPPKVVDKAKSPGVDPKQLAARLQKVSL 4531	
È	792	STRAIN=Bristol N2; Fulton L., Waterston
අු	4532 QQSPLVMSSVVKKQAHAHSGPTSAGSSSVPSFQQPGSPSVSKKKHGGSKPTDVSKTASHP 4591	
ò	814 LSGQLSIKLWFDKVGHQLIVTILGAKDLPSREDGRPRNPYVXIYFLPDRSD 864	CC -i- SIMILARITY: Contains 1 FYVB-type zinc finger. CC -i- SIMILARITY: SOME, TO YEAST YNLOBYW.
쉺	4592 ITGELQLQINYD-LGN-LIIHILQARNLVPRDNNGYSDPFVKVYLLEGRGQVMVVQNASV 4649	This SWISS-PROT entry is copyright. It is produced through
È	865 KNKRRIKIVKKILEPKWNQTFIYSPVHRREFRERMLEITLWDQARVREESBFLGBILLE 924	
Ор	4650 BYKRIKYVQKSLNPEMNQTVIYKSISMEQLMKKTLEVTVWDYDRFSSNDFLGEVLID 4707	CC modified and this statement is not removed. Usage by and
È	PLPRPSPYLPRROLHGES - PTRRLORS	- 5.
a	4708 LSSTSHLDNTPRMYPLKEQTESIEHGKSHSSQMSQQSFKPS 4748	
ò	981 VSDYDCEDGVGVVSDYRHNGRDLQSSTLSVPBQVMSSNHCSPSGSPHRVDVIGRTRSMSP 1040	- 1,
đ	4749VIXSRSHGIPPDPSXDMQVPTIBKSHSSPGSSKSSBGHIRSHGP 4793	WormPep; F37A4.7; CE(InterPro; IPR000008;
Š	1041 SAPPPQRNVBQGHRGTRATGHYNTISRMDRHRVMDDHYSSDRDRDCEAADROPYHRSRST 1100	
д	4794 SRSQSKTSVAQTH	IPR001565; Synapt
ò	SKRDDTH MRSMDSI MTGBSADDSDAG COGUDGOTO	
i É	::	DR PRINTS; PR03518; RPH3A effector; 1. DR PRINTS; PR00360; C2DOWAIN.
g ,	1624TXPIN 4833	DR PRINTS; PR00399; SYNAPTOTAGMN. DR SMART; SM00219; C2: 2
È	1161 GTGRRGRQLPQLPPKGTLERSAMDIEERNRQMKLNKYKQVAGSDPRLEQDYHSKYRSGWD 1220	
đ	4834 4833	DR PROSITE; PS50104; CZ DOWAIN 2; 2.
à	1221 PHRGADT-VSTKSSDSDVSDVSAVSRTSSASRFSSTSYMSVQSERPRGNRKISVFTSKMQ 1279	
ορ	4834 -HRPAETSVSTGSSGSSVGSGYSVDSE4859	847 987
ò	1280 NRQMGVSGKNLTKSTSISGDMCSLEKNDGSQSDTAVGALGTSGKKRRSSIGAKMYAIV 1337	SEQUENCE 1021 AA; 11174
đ	4860GSSCVAGEPNILPIPRIGOGODPVKOPGWGA 4894	Query Match 4.1%; Score 338; DB 1; Length 1021 Best Local Similarity 20 08; Dred No. 1. 10
ò	SASS	rative 139; Mi
ą	4895	QY 90 KQPNEKEPQTKLHQQFRMYKEQVKKMGRESQQQQQQX
È	TOTAL TOTAL A CONTRACT TO A CO	DD 114 RSPINSKAQIGSITAARQRHIQKVLAKAERSKSKEQQRIGKNVDRLEKO
ÿ	DOMITE FOVOLANDOY FOLKING LOFAND VORQITAL PANGDIQ VORMIDROVQUEVEITR	Qy 131 T-CGICHKTKPADGCGHNCSYCOTKFCAR-CGGRVSIRENKV-
3 (4321QLIVEILQ 4928	DD 172 THCLLCH-TEPGLIASKSYAAMCUDGREVVOORNOTURETURATURATURATURATURATURATURATURATURATURA
Š	1458 ARGLVVKPGSKT-LPAPYVKVYLLDNGVCIAKKKTKVARKTLEPLYQQLLSFESSPQG 1514	
අ	4929 CRNITYKFKSPDHLPDLYVKIYVINIATQKKVIKKKTRVCRHDREPSFNETFRFSLSPAG 4988	
ò	1515 RVLQIIVMGDYGRMDHKSFMGVAQILLDBLELSNMVIGWFKLFPPSSLVDFT 1566	100
qq	4989 HSLOILLFSNGGKFMKKTLIGEACIWLDKVDLRKRIVNWHKLLVSFT 5035	

PRT; 1021 AA.

RESULT 5

YPT7 CAREL

1D YPT7 CAREL

STANDARD;

1AC P41885;

DT 01-NOV-1995 (Rel. 32, Created)

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      131 T-CGICHKTKP----ADGCGHNCSYCQTKFCAR-CGGR---VSIRENKY--MWVCMLCRK 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               180 QOBIL-TKSGAMFYNSGSNTLQOPDOKVPRGL---RNEEAPORKKAKLHBOPOPGAPG- 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  231 ARBVLWKKSGAWFYKE-MPEPQRPDDRLPYYVPVTYNGTLFNASSA---ATPLSGTPGG 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      235 ----DLSVPAVE-----KGRAHGLTRODTIKNGSGVKHQIASDWPSDRKRS----- 276
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       342 PPRSSSDGESFVQSGVPRRALNNKTPVGSTSATTSPAPPTSTTPTSRR-----A 392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              277 -PSVSRDQNRRYEQSEEREDYSQYVP----SDGTMPRSPSDYADRRSQREPQFYEEPGHL 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      332 NYRDSNRRGHRHSKEYIVDDEDVESRDEYERGRREEEYQARYRSDPNLARYPVKPQPYEE 391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          tch 4.1%; Score 338; DB 1; Length 1021; al Similarity 20.9%; Pred. No. 6.1e-09; Indels 266; Gaps 197; Conservative 139; Mismatches 342; Indels 266; Gaps
IN-Eristol N2;
on L., Materston R.;
ditted (FEB-1994) to the EMBL/GenBank/DDBJ databases.
SIMILARITY: Contains 2 C2 domains.
SIMILARITY: Contains 1 FYVE-type zinc finger.
SIMILARITY: SOME, TO YEAST YNLOSTW.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       168 233 FYVE-TYPE.
758 847 C2 DOMAIN 1.
898 997 C2 DOMAIN 2.
1021 AA, 111749 MW; 947C38B7C37BA462 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                terPro; ITRO00008; C2.
tterPro; ITRO00008; C2.
tterPro; ITRO00149; LRI.
tterPro; ITRO00149; LRI.
tterPro; ITRO001315; RPH3A effector.
tterPro; ITRO001315; RPH3A effector.
tterPro; ITRO00136; Zuf_FYVB.
terPro; ITRO00136; Zuf_FYVB.
im; PP00168; C2; Z.
im; PP00168; C2; Z.
im; PR00189; C2; DOMAIN.
INTS; PR00199; C2 DOMAIN.
INTS; PR00199; C3 DOMAIN.
INTS; PR0
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P47709; 1ZBD.
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J. Invest. Dermatol. 101:658-718(1993)

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                                      434
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                                                                                              QMRIHABVSRARHERRHSDVSLANAELEDSRISLLRMDRPSRQRSVSERRAAMENQRSYS
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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MEDLINE=93315897; PubMed=7686953;
O'Keefe E.J., Hamilton E.H., Lee S.-C., Steinert P.M.;
"Trichohyalin: a structural protein of hair, tongue, nail, and
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
             FUNCTION: INTERNEDIATE FILAMENT-ASSOCIATED PROTEIN THAT ASSOCIATES IN REGULAR ARRAYS WITH ERRATIN INTERNEDIATE FILAMENTS (KIF) OF THE INNER ROOT SHEATH CELLS OF THE HER FOLLICLE AND THE GRANULAR LAYER OF THE RECOMES CROSS-LINKED TO KIF BY ISODIPPETIDE BONDS. IT MAY SERVE AS SCAPPOLD PROTEIN, TOGETHER WITH INVOLUCIRIN, IN THE ORGANIZATION OF THE CELL ENVELOPE OF EVEN ANCHOR THE CELL ENVELOPE TO THE KIF NETWORK. IT MAY BE INVOLVED IN ITS OMN CALCIUM-DEPENDENT POSTSYNTHETIC PROCESSING DURING TERMINAL
                                                                                                                                                                                                                                         -i- SUBUNIT: Monomer (Probable).
-i- TISSUE SPECIFICITY: FOUND IN THE HARD KERATINIZING TISSUES SUCH AS THE INNER ROOT SHEATH (IRS) OF HAIR FOLLICLES AND MEDULLA, AND IN THE FILIFORM PAPILLAE OF DORSAL TONGUE RFITHELIUM (PROBABLE).
-i- DEVELOPMENTAL STAGE: EXPRESSED DURING LATE DIFFERENTIATION OF THE EPIDERMIS.
                                                                                                                                                                                                                                                                                                                                                                                         -!- DOWAIN: CONSISTS OF NINE DOWAINS. DOWAIN I CONTAINS TWO EF-HAND CALCIUM-BINDING DOWAINS. DOMAINS 2-4, 6, AND 8 ARE ALMOST RETICAL. CONFIGURED & A SERIES OF PEFFIDE REPEATS OF VARYING REGULARITY, AND ARE THOUGHT TO FORM A SINGLE-STRANDED ALPHA-HELICAL ROD STABILIZED BY IONIC INTERACTIONS. DOWAINS 5 AND 7 ARE LESS WELL ORGANIZED AND MAY INDUCE FOLDS IN THE MOST REGULAR AND MAY BIND KIP DIRECTLY BY IONIC INTERACTIONS. DOWAINS 5 AND 7 ARE LESS WELL ORGANIZED AND MAY INDUCE FOLDS IN THE MOST SECIES.

-!- FTM: SUBSTRATE OF TRANSCLUTAMINASES, SOME 200 ARGININES ARE PROBABLY CONVERTED TO CITRULLINES BY PEFFIDYLARGININE BENIDASE.
-!- SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE S-100
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9 X 6 AA TANDEM REPEATS OF R-R-E-Q-Q-L.
2-2.
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EF-HAND 2 (HIGH AFFINITY) (POTENTIAL)
6 X 13 AA TANDEM REPEATS OF
R-R-B-Q-E-B-E-R-R-R-Q-L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESP, PO2633, 41CB.
RESP, PO2633, 41CB.
RESP, PO2633, 41CB.
RESP, PO2633, 41CB.
RESP, PO2633, 41CB.
RESP, PO2633, 41CB.
RESP, PO2690, 61CB.
RESP, PO2690, 61CB.
RESP, PO2690, 61CB.
RESP, PO2690, 61CB.
RESP, PR0020151, CaBP S100.
RESP, PER0020171, Spectrin.
RESP, PER00203, 61CB.
RESP, PER00203, 61CB.
RESP, PER0036, 61CB.
RESP, PO2696, 
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	09 096 YRHNGRDLQSSTLSVPEGVMSSNHCSPSGSPHRVDVIGGETRSNGPSAPPPGRAVGG 1052 1012	RESULT 7 RP3A HUMAN ID R973 HUMAN STANDARD; PRT; 694 AA. O9Y2JO; Q96ABO; DT G-OCT-2001 [Rel. 40, Last sequence update) DT 16-OCT-2001 [Rel. 42, Last annotation update) DT 16-OCT-2003 [Rel. 42, Last annotation update) DR Rabphilin-3A. RAPIA OR KIAA0985. GW RFH3A OR KIAA0985. OC Mammalia; Butheria; Craniata; Vertebrata; Buteleostomi; OC Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo. OC Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo. OC Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo. NCB1 TaxiD=9606; RN [1] RP SEQUENCE FROM N.A. RN Nagaes T.; Ishikawa KI.; Suyama M., Kikuno R., Hirosawa M., RA Miyajima M., Tanaka A., Kotani H., Nomura M., Ohara O.; RY Miyajima M., Tanaka A., Kotani H., Nomura M., Ohara O.; RY The complete sequences of 100 new cDNA clones from brain which code for large proteins in vitro."; RN SEQUENCE FROM N.A. RN SEQUENCE FROM N.A.
FT REPEAT 427 432 2-7. FT REPEAT 433 438 2-8. FT DOMAIN 444 702 9 X 28 AA APPROXIMATE TANDEM REPEATS. FT DOMAIN 923 1162 8 X 30 AA TANDEM REPEATS. FT REPEAT 923 952 4-1. FT REPEAT 983 1012 4-2. FT REPEAT 1013 1042 4-4. FT REPEAT 1072 4-4. FT REPEAT 1072 4-6. FT REPEAT 1103 1102 4-6. FT REPEAT 1103 1132 4-7. FT CONFLICT 1754 1801 Q 23 X 26 AA APPROXIMATE TANDEM REPEATS. FT CONFLICT 1754 1801 Q 29 X 37 X 3	Similarity 17.4%; Sconsorvative 213; Pres. S. Conservative 213; Pres. S. Co	356 SRDB-YERGRREEFYQARYRSDPNLARYPVKPQPYERGWRIHAEVSRARHERRHSDVSLA 414 533 RREQRIEKRQEEERILQORLARSCOLRR 586 415 NARLEDSRISLLEMDRPSRQORSVERRRAAMENQRSYSMERTREAGCQSSYPQRISHEDP 474 587 KREGEERPQLLKREERRRQORLKREGERLEGR-LKREEVERLEGERRERDERLEGERREGEL- 586 415 NARLEDSRISLLEMDRPSRQORSVERRAAMENQRSYSMERTREAGCQSSYPGRTSHEDP 474 587 KREGEERPQLLKREEERRQORLKREGERLEGR-LKREEVERLEGERRERDERLEGERSPERFREGER- 688 H

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GRVSLRSNKVMWVCNLCRKQQBILITKSGAWFYNSGSNTLQQPDQKVPRGLRNBEAPQEKK 220
                                                                            128 VETNNRLHSV-WLCKICIEGREVWRRSGAWFEKG-----FFRGVLPQ------PMPIK 173
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70 - EMEQERIGRLVDRLENMRKNVAGDGVNRCILCGEQLAMLGSAC-VVCEDCKKNVCTKCG 127
                                                                                                                                                                                                                                                                                                                199 -------RAPARGDSEDRRGEDSEDRAGE 231
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Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
NCBI_TaxID=10090;
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28-FEB-2003 (Rel. 41, Last annotation update)
Rabphilin-3A.
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                                   A Straubberg R.L., Feingold R.A., Grouse L.H., Derge J.G.,

A Itachins S.F., Zeeberg B. S., Wagner L., Schaefer C.R., Schuler G.D.,

A latechul S.F., Zeeberg B. Buetow K.H., Schaefer C.F., Bhat N.K.,

A latechul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Hopkins R.F., Jordan H., Moore T., Max S.I., Mang J., Haich F.,

A stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

B capleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Raha S.S., Worley N.A., McKernan K.J., Malek J.A., Gunarathe P.H.,

Richards S.W., Worley M.C., Hale S., Garcia A.M., Gabb R.A.,

Richards S.W., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

Rullalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

Rullalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

Rulting M.M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Bronerch A., Schein J.S.A., Jones S.J.M., Marra M.A.;

Receneration and initial analysis of more than 15,000 full-length

Proc. Natl. Acad. Sci. U.S.A., 99:16899-16903(2002)

PROTEIN RAB-3A IN SYNAPTIC VESICLE TRAFFIC AND/OR SYNAPTIC

VESICLE FUSION: COULD FLAY A ROLE IN NEUROTRANSMITTER RELATED

PROTEIN RAB-3A IN SYNAPTIC VESICLE TRAFFIC AND/OR SYNAPTIC

VESICLE FUSION: COULD FLAY A ROLE IN NEUROTRANSMITTER RELATED

REGILATING MENGRANG FLOW IN THE NERVE TERMINAL (BY SIMILARITY).

C. -- SIMILARITY: Contains 1 FYVE-type zinc finger.
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|DRQRKQBE-----LIDEEK------BIINRVIARAEKME-----
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PROSITE; PSO0499; C2 DOMAIN 2; 2.
PROSITE; PSS0049; C2 DOMAIN 2; 2.
PROSITE; PSS0178; ZF_FYVE; 1.
Repeat; Synapse; Profein transport; Zind-finger.
DOMAIN 1 275 RAB P25/SMG P25A BINDING (GTP GAMMA-S-
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555 C2 DOMAIN 2.
100 NDXRO -> K IN REF 2).
76872 MM; BD9C43F306A04D69 CRC64;
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InterPro; IPR001565; Synaptotagmin.
InterPro; IPR000306; Znf FYVB.
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Pfam; PF02318; RPH3A_effector; 1.
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PRINTS; PR00399; SYNAPTOTAGMN.
SMART; SM00239; C2; 2.
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InterPro; IPR002149; LR1
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694 AA;
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PSVSRDQNRRYEQSBEREDYSQYVPSDGTMPRSP8---DYADRRSQRB---PQFYBEPGHL 331
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                                                                                                                                                                                                             332 NY-----RDSNRRGHRHSKEYIVDDEDVESRDEYERQ----RREREYQA
                                                                                                                                                                                                                                                                       225 SHGPPTRRASEARMSTAARDSEGNDHAHG------GGTGDTSKSPAGLRRANSVQA
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
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01-FEB-1996 (Rel. 33, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
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                    165 QPMPIKKTKPQQPAGBPA-----
                                                                                                                                                                                                                                                                                                                                                   372 RYRSDPNLARYPVKPQP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD:
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RP3A RAT
ID RP3A RAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the EMBL outstation the European Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licenseelsb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          101 LHOOFEMYKEQVKKMGER----SQOQQEQKGDAPTCGICHKTKFADGCGHNCSYCQTKFC 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       75 LVDRLETMRKNVAGDGVNRCILCGEQLGMLGSA--CVVCED-------CKKNVC 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            157 ARCGGRVSLRSNKVMWVCNLCRKQQRILITKSGAWFYNSGSNTLQQPDQKVPRGLRNERAP 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  120 TKCGVETSNNRPHPVWLCKICLBQREVWRKSGAWFF------KGPPKQVLF 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           217 QEKKAKLHEQPQFQGAPGDLSVPAVEKGRAHGLTRQDTIKNGSGVKHQIASDMPSDRKRS 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             35 AQTDRQRKQEB------ITDEEK------EIINRVIARAEKMEAMEQERIGR 74
                                                                                                                                                                                                                                                                                                                                  cells.";
J. Biochem. 116:239-242(1994).
-!- FUCTION: PROTEIN TRANSPORT, PROBABLY INVOLVED WITH RAS-RELATED PROTEIN RAB-3A IN SYNAPTIC VESICLE TRAFFIC AND/OR SYNAPTIC VESICLE FUSICLE FUSICLE FUSICLE FUSICLE FUSICE FUSIC ON THE NEW TERMINAL.
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Matches 176; Conservative 106; Mismatches 293; Indels 370; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PSSO049; C2 DOMAIN 1; 2.
PROSITE; PSSO0049; C2 DOMAIN 2; 2.
PROSITE; PSSO178; ZF PYVE; 1.
Repeat; Synapse; Protein transport; Zinc-finger.
DOMAIN 1 274 RAB P25/SMG P25A BINDING (GTP GAMMA-S-BOUND).
                                                                                                                                                             SEQUENCE OF 1-606 FROM N.A.
STRAIN=CSTSL/6;
MEDLINES-912244; PubMed=7822236;
Inagaki N., Mizuta M., Seino S.;
"Cloning of a mouse Rabphilin-3A expressed in hormone-secreting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3.2%; Score 264; DB 1; Length 681; 18.6%; Pred. No. 1.2e-05;
                                                                    Inagaki N.,
Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -i- TISSUE SPECIFICITY: Specifically expressed in brain.
-i- SIMILARITY: Contains 2 C2 domains.
-i- SIMILARITY: Contains 1 FYVB-type zinc finger.
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C2 DOMAIN 1.
C2 DOMAIN 2.
D09F8DBD2CBB271E CRC64;
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InterPro; IPR000008; C2.
InterPro; IPR00149; LRI.
InterPro; IPR00149; LRI.
InterPro; IPR001565; SynapCotagmin.
InterPro; IPR001565; SynapCotagmin.
InterPro; IPR001565; SynapCotagmin.
InterPro; IPR00186; Zaf PrvB.
Fam; PF00168; C2; Z.
Pfam; PF00188; RPH3A effector; I.
PRINTS; PR001399; SYNAPTOTAGMN.
SWART; SM00239; C2; Z.
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75489 MW;
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361
485
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539 6
681 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P47709; 1ZBD.
SEQUENCE FROM N.A.
                              STRAIN=C57BL/6;
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DOMAIN
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LHQQFEMYKEQVKRMGEB----SQQQQEQKGDAPTCGICHKTKFADGCGHNCSYCQTKFC 156
                                                   -----CHCRIVC 119
                                                                                                         120 TKCGVETSNNRPHPVWLCKICLEGREVWKRSGAMPF------KGPPKQVLP 164
                                                                                                                                            QEKKAKLHEQPQPQAPGDLSVPAVEKGRAHGLTRQDTIKNGSGVKHQIASDMPSDRKRS 276
                                                                                                                                                                                                         PSVSRDQNRRYEQSEEREDYSQYVPSDGTMPRSPS--DYADRRSQRE---PQFYEEPGHL 331
                                                                                                                                                                                                                                       194 PA-----RAPARGDMEDRRAPGGKPGPDLTSAPGRG 224
                                                                                                                                                                                                                                                                                                      225 SHGPPTRRASBARMSTTTRDSBGWDHGHG-----GGAGDTSRSPGGBGGLRRANSVQAS- 278
                                                                                                                                                                                                                                                                                                                                                                     279 RPAPASMPSPAPPOPVQPGPPGGSRAAPGPGRFPEOST-----KAPPSDPGYPGA 328
                                                                                                                                                                                                                                                                                                                                                                                                                                477 RRSPIPLDRPDWRRADSLRKQHHLDPSSAVRKTKREKWETWLRNDSLSSD-QSESVRPPP 535
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             536 PRPHKSKKGGKWRQVSLSSSEBELASTPEYTSCDDVELESESVSEKGDSQKGKRKTSEQG 595
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             596 VLSDSNIRSERQKKRMYYGGHSLEEDLEMSEPQIKDSGVDTCSSTTLMBEHSHSDKHPVT 655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  S62 IRCVHLAAMDANGYSDPFVKLMLKFDMGKKAKHKTQIKKKTLMPEFNEEFFTDIKH-SDL 620
                                                                                                                                                                          165 OPMPIKKTKPOOPAGEPA------TOBSPH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   359 ARQPPPAEEEE-----EBANSYDSDQA---TTLGALEFBLLYDQDNSNLQCTIIRAKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       409 LKPMDSN-----GLADPYVKCHILLP------GRASKSNKLRTK---
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                                                                               ARCGGRVSLRSNKVMWVCNLCRKQQEILTKSGAMFYNSGSNTLQQPDQKVPRGLRNEEAP
                                                                                                                                                                                                                                                                        417 ELEDSRISLIRMDRPSRORSVSERRAAMENORSYSMERTREAQGOSSYPORTSNHSPPTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADTVGHLRPGDEVLEWNGRLLQGATFREVYNIILBSKPRPQVELVVSRPIGDIPRIPDST
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                                                                                                                                                                                                                                                                                                                                    374 REDPNLARYPVKPQP-----YEBOWRIHARVSRARHERRHSDVSLANA
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                621 AKKSLDISVMDYD--IGKSNDYIGGCQLGI-SAKGERLKENYE 660
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                                               75 LVDRLETMRKNVAGDGVNRCILCGBQLGMLGSA--CVVCED-
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Last annotation update)
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(Rel. 33,
(Rel. 40,
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Q06846;
01-FEB-1996 (Rv
01-FEB-1996 (Rv
16-OCT-2001 (Rv
Rabphilin-3A.
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                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the RMBL outstation the buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lib.sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       42 AVMDROKKEBEKEQSVLKIKEEHKAQPIQWFPFSGITELVNNVLQPQQK-QPNEKEPQTK 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels 363; Gaps
                                                                                                        Cell 96:363-374(1999).
-!- FUNCTION: PROTEIN TRANSPORT. PROBABLY INVOLVED WITH RAS-RELATED PROTEIN RAB-3A IN SYNAPTIC VESICLE TRAPFIC AND/OR SYNAPTIC VESICLE TRAFFIC AND/OR SYNAPTIC VESICLE PUSICIE FUSION. COULD PLAY A ROLE IN NEUROTRANSMITTER RELEASE BY REGULATING MEMBRANE FLOW IN THE NERVE TERMINAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PS00499; C2 DOMAIN 1; 2.
PROSITE; PS50004; C2 DOMAIN 2; 2.
PROSITE; PS500178; ZE FYVE; 1.
PROSITE; PS50178; ZF FYVE; 1.

DOMAIN 1 277 RAB P25/SMG P25A BINDING (GTP GAMMA-S-BOMAIN)
                                                                of
                                      Ostermeier C., Brunger A.T., "Structural basis of Rab Aff.; "Structural basis of Rab effector specificity: crystal structure the small G protein Rab3A complexed with the effector domain of rabphilin.3A.", Cell 96:363-374 (1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 684;
                                                                                                                                                                                                        TISSUE SPECIFICITY: Specifically expressed in brain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            75832 MW; 05838BC3C7A86444 CRC64;
                                                                                                                                                                                                                     -!- SIMILARITY: Contains 2 C2 domains.
-!- SIMILARITY: Contains 1 FYVE-type zinc finger.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
3.2%; Score 202.7, ----,
Best Local Similarity 18.8%; Pred. No. 1.4e-05;
Matches 177; Conservative 105; Mismatches 298;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRO-RICH.
C2 DOMAIN 1.
C2 DOMAIN 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PYVE-TYPE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Interpro; 1PR000008; C2.
Interpro; 1PR002149; LRI.
Interpro; 1PR003315; RPH3A_effector.
Interpro; 1PR001565; Synapcotagmin.
Interpro; 1PR000306; Znf_FYUE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00168; C2; 2.
Pfam; PF00168; C2; 2.
Pfam; PF00318; RPH3A_effector; 1.
PRINTS; PR00369; C2DOMAIN.
SMART; SM00239; C2; 2.
                                                                                                                                                                                                                                                                                                                                                                                               EMBL; U12571; AAA62662.1; -. PIR; I58166; I58166.
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                                                                                                                                                                                         SUBUNIT: Monomer
                                                                                                                                                                                                                                                                                                                                                                                                                              PDB; 1ZBD; 12-APR-99
PDB; 3RPB; 23-DBC-99
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128 VETSNNRPHPVWLCKLCIEQREVWKRSGAMFFKG-----FFKQVLPQ------PMPIK 174
              GRVSLRSNKVMWVCNLCRKDORILTKSGAMFYNSGSWTLQOPDOKVPRGLRNERAPORKK 220
                                                                                                                                                                                                                                  SPSVSRDQNRRYEQSEEREDYSQYVPSDGTMPRSPSDYADRRSQREPQFYKEPGHLNYRD 335
                                                                                                                                                                                                                                                                                                                                                    SNRRGHRHSKEYIVDDEDVESRDEYERQRREBEYQARYRSDPNLARYPVKPQPYERGMRI 395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  396 HAEVSRARHERRHSDVSLANAELEDSRISLLRMDRPSRQRSVSERRAAMENQRSYSMERT 455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ---- GOPGPPGGSRPSPGPIGK--- PPDQRPEVADSDP----- DYTGAAAQPRERTG 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            343 GIGGYSAAGTREDRAGHPPGSYTQASAAPQPVVASARQPPPBEBERKAN----SYDSD 398
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                                                                                                                                                              175 KNKPQQPVSEPVPA-APEPATPEPKHPARAPTRGDT-EDRRGPGQKTGPDMTSAPGRGSY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    456 REACGOSSYPORTSNHSPPTPRRSPIPLDRPDWRRADSLRKOHHLDPSSAVRKTKREKME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     516 TMLRNDSLASDQSESVRPP------PPRPHKSKKGGKMRQVSLSSS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           503 ------PIGE-----TRPSLKKLKDNQRKNFNIC--LERVIPMKRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   717 DIVGHLRPGDEVLEWNGRLLQGATFEEVYNIILESKPEPQVELVVSRPIGDIPRIPDSTH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    233 GPPVRRASEAR--MSSSGRDSDSWDQCHCMCAGDPS-------QSPAGL
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  642 KKSLDISVWDYD--IGKSNDYIGGCQLGI-SAKGERLKHWYE 680
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SEQUENCE FROM N.A.
MEDLINE=91335210; PubMed=1651562;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Skropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licenseelsb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=94086530; PubMed=8262955; Yakai W., Nishikawa J., Yamaguchi T., Shirataki H., Kishida S., Miyazaki M., Nishikawa J., Yamaguchi T., Shirataki H., Takai Y., Takai Y., Wada K., Numata S.-I., Kaibuchi K., Takai Y., Takai Y., Wayai W., Walai W., Walai W., Takai Y., Takai Y
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PROSITE; PSO0499; CZ DOWAIN 1; 2.
PROSITE; PSSO049; CZ DOWAIN 2; 2.
PROSITE; PSSO0178; ZF_FYVB; 1.
Repeat; Synapse; Protein transport; Zind-finger.
DOWAIN 1 280 RAB P25/SMG P25A BINDING (GTP GAMMA-S-BOMAIN)
Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                            Shirataki H., Kaibuchi K., Sakoda T., Kishida S., Yamaguchi T., Wada K., Miyazaki M., Takai Y., "Rabhilin-3A, a putative target protein for smg p25A/rab3a p25 GTP-binding protein related to synaptotagmin.";
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Conservative 112; Mismatches 307; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE SPECIFICITY: Specifically expressed in brain. SIMILARITY: Contains 2 C2 domains. SIMILARITY: Contains 1 FYVE-type zinc finger.
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417 508 C2 DOMAIN 1.
577 665 C2 DOMAIN 2.
704 AA; 77977 MW; 1324D048F5F8FFD4 CRC64;
                                                                                                        SECUENCE FROM N.A., AND PARTIAL SECUENCE TISSUE=Brain;
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InterPro; IPR000008; C2.
InterPro; IPR00149; LRI.
InterPro; IPR00315; RPH3A_effector.
InterPro; IPR001565; Synaptotagmin.
InterPro; IPR001665; Synaptotagmin.
                                                                                                                                                                    MEDLINE=93204952; PubMed=8384302;
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PRINTS; PR00399; SYNAPTOTAGMN.
SMART; SM00239; C2; 2.
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                          Bovidae, Bovinae, Bos.
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Pfam; PF02318; RPH3A
Eutheria;
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172; Conserv
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MEDLINE-97094176; PubMed-8940264;
BCcles D.M., van der Luijt R.B., Breukel C., Bullman H., Bunyan D.,
Fisher A., Barber J., du Boulay C., Primrose J., Burn J., Fodde R.;
"Hereditary desmoid disease due to a frameshift mutation at codon 1924
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=20243021; PubMed=10782927; Couture J., Mitri A., Lagace R., Smits R., Berk T., Bouchard H.-L., Fodde R., Alman B., Bapat B., Agermine and of the APC gene results in a severe desmoid phenotype and is associated with overexpression of beta-catenin in the desmoid tumor.";
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Day C.L., Alber T.;
"Crystal structure of the amino-terminal colled-coll domain of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             X-RAY CRYSTALLOGRAPHY (3.1 ANGSTROMS) OF 1021-1035 IN COMPLEX WITH
Kinzler K.M., Nilbert M.C., Su L.-K., Vogelstein B., Bryan T.M., Levy D.B., Smith K.J., Preisinger A.C., Hedge P., McKechnie D., Finniear R., Markham A., Groffen J., Boguski M.S., Altschul S.F., Horil A., Ando H., Miyoshi Y., Miki Y., Nishisho I., Nakamura Y.; "Identification of FAP locus genes from chromosome 5q21."; Science 253:661-665(1991).
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Vogelstein B., Kinzler K.W.;
"Association of the Abc tumor suppressor protein with catenins.";
Science 262:1734-1737(1993).
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                                                                                                                                                                    MEDLING=91330307; PubMed=1678319; Jostyn G. Carlson M., Thliveris A., Albertsen H., Gelbert L., Samowitz M., Groden J., Stevens J., Spirio L., Robertson M., Sargeant L., Krapton K., Molff B., Burt R., Hughes J.P., Warrington J., McPherson J.D., Wasmuth J., Le Paslier D., Abderrahim H., Cohen D., Leppert M., White R.; "Identification of deletion mutations and three new genes at (familial polyposis locus.";
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Eklof Spink K., Fridman S.G., Weis W.I.;
"Molecular mechanisms of beta-catenin recognition !
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                                                                                                                                    SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
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                                                                                                                            VARIANTS COLORECTAL CARCINOMA THR-880; ILB-890 AND VAL-1508.
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3.1%; Score 258.5; DB 1; Length 2843;
Best Local Similarity 17.9%; Pred. No. 0.00014;
Matches 304; Conservative 238; Mismatches 618; Indels 535;
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Mutat. 9:7-16(1997).
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                   GAXSPSKSGAQTPXSPPRHYVQRTPLMFSRCTSVS---SLDSFRSRSIASSVQSEPCSG
                                                        -----GQSSYPORTSNHSPPTPRRSPIPLDRPDWRRADBLRKGHHLDPSSAVRKTKRBK
                                                                                                                                   | : | : :::: | | | : ::: | | | | 1452 ----VRNIKAPTAERRES------GEKQAAVRAAVQRVQVLPDADILLHFATESTPDGFSC
                                                                                                                                                                                                                                                      691 KVVGGKMTESGRLCARITKVKKGSLADTVGHLRPGDEVLENNGRLLQGATFEEVYNIILE
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                                                                                                                                                                          D-----BSESVSERGDSQ-RGRRYT--SEGG
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RESOURNCE OF 1-1190 FROW N.A. (ISOFORMS 1; 2 AND 4).

RECORDING=22554683; PubMed=12466851;

REMINE=22554683; PubMed=12466851;

REMINE=22554683; PubMed=12466851;

RAD ANGERINE=22554683; PubMed=12466851;

RAD ANGERINE T., Adachi J., Bono H., Kondo S.,

RAD ANGERINE T., Assubawa T., Adachi J., Bono H., Kondo S.,

RAD ANGERINE T., Hasegawa Y., Nogami A., Schombach C., Gojobori T.,

RAD Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,

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RAD Baldarelli R., Bradt D., Brusic V., Chothia C., Corbani I.E., Cousins S.,

RAD Baldarelli R., Fletcher C.P., Forrest A., Frazer K.S.,

RAD Baldarelli R., Gariboldi M., Glssi C., Godzik A., Gough J.,

RAD Balda B., Dragani T.A., Fletcher C.P., Forrest A., Gough J.,

RAD Anai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,

Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,

RAD ANGASAHMA T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,

RAD RA, Ravasi T., Reed J.C., Reed D.J., Reid J., Ramachandran S.,

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RAD RA, Schneider C., Semple C.A., Serou M., Shimada K.,

RA, Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,

Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang I.,

RA, Hincane-Kishikwa T., Komo H., Nakamura M., Sakazume N., Sato K.,

RA, Saltaki T., Waki K., Kawai D., Alzawa K., Shinagawa I.,

RA, Hara A., Hashizume W., Imocani R., Ishii Y., Itoh M., Kagawa I.,

RA, Wasunishi A., Yoshino M., Raterston R., Shinagawa A.,

RA, Wasunishi A., Yoshino M., Raterston R., Shinagawa A.,

RA, Saunishi A., Yoshino M., Raterston R., Shinagawa A.,

RA, Ravashino M., Rayanino M., Rayanishi A., Sakarino M.,

RA, Sasunishi A., Yoshino M., Raterston R., Shinagawa I.,

RA, Rayanishi A., Yoshino M., Raterston R., Shinagawa I.,

RA, Rayanishi A., Yoshino M., Raterston R., Shinagawa I.,

RA, Rayanishi A., Yoshino M., Rayanishina M.,

RA, Rayanishi A., Yoshina M., Rayanishina M.,

RA, Rayanishi A.
2320 PIQSPGRNSISPGRNGISPPNKLSQLFRISSPSTASTKSSGSGKGKS-YTS--PGRQM--S 2374
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                                                                                                                                    2375 QONLITKOTGLSKNASSIPRSESASKGLNOMNNGNGANKK------VELSKNSSTK 2423
                                                                                1287 GKNITKSTSISGDMCSLEKNDGSQSDTAVGALGTSGKKRRSSIGAKMVAIVGLSRKSRSA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mamoru A., Setsuko S., Yoshihide T.; "Molecular cloning of murine acinush, a gene for apoptotic chromatin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. (ISOFORMS 2 AND 3).
MEDLINE=99418558; PubMed=10490026;
Sahara S., Aoto M., Eguchi Y., Imamoto N., Yoneda Y., Tsujimoto Y.;
"Acinus is a caspase-3-activated protein required for apoptotic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACIN_MOUSE STANDARD; PRT; 1338 AA.
Q9JIX8; Q9CSN7; Q9CSN7; Q9R046; Q9R047;
28-FRBL-2003 (Rel. 41, Created)
28-FRBL-2003 (Rel. 41, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Apoptotic chromatin condensation inducer in the nucleus (Acinus).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             condensation.";
Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                            IsoId-Q9JIX8-4; Sequence-VSP 004032; PTM: Undergoes proteolytic cleavage; the processed form is active, contrary to the uncleaved form (By similarity). SIMILARITY: Contains 1 SAP domain. CAUTION: Ref. 2 sequence differs from that shown due to frameshifts in position 110 and 112.
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R (IN REF. 3; BAB28030)
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B912D9CB5750FBF4 (RC64;
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(IN REF. 1, AAD56723)
                                                                                                                                                      Name=2; Synonyms-S;
IsoId=Q9JIX8-2; Sequence=VSP_004030, VSP_004033;
Name=3; Synonyms-S';
IsoId=Q9JIX8-3; Sequence=VSP_004031;
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EMBL; AF124729; AAD56727.1; -...
EMBL; AF168782; AAF89661.1; ALT FRAME.
EMBL; AK011698; -; NOT ANNOTATED_CDS.
EMBL; AK012099; BAB28030.1; -...
EMBL; AK012337; BAB28171.2; -...
EMBL; AK050467; BAC34272.1; ALT_INIT.
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GO; GO:0005730; C:nucleolus; IDA.
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InterPro; IPR003034; SAP.
Pfam; PF02037; SAP; 1.
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PROSITE; PS50800; SAP; 1.
Apoptosis; Nuclear protein;
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ខេត	the European Bioinformatics Institute. There are no restrictions on its	ð	486 POWRRADSLE
ខខ	modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.ich.st.ch.nhamannon/	a	1091 ADVEALQAAN
ខូខូ	or send an email to licenseelsb-sib.ch).	è	516 TMLRNDSLS
n n	EMBL; X66397; CAA47021.1; EMBL; Y00672; CAA68681.1;	Q Q	1151 DLEKONRLLE
S S	Genew; HGNC:12017; TPR MIM: 189940: -	ò	258BL
D DR	GO; GO:0005737; C:cytoplasm; TAS. GO: GO:0005643; C:miclast nove: mag	a	1208 BIAETRFEVA
i i i i	GO; GO:0006606; P:protein-nucleus import; TAS.	ò	593 ROGVLSDSNT
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FT	1476 1595 COLLED COLL 527 530 POLY-SER	4	1427 KVKTITQVKK
r r	1833 1836 1957 1964	ò	776 HAQLESSSS
SO	2295 2298 CE 2349 AA; 265600 M	<u>유</u>	1483 LNQARTKSKS
One	3.1%; Score 255.5; DB 1;	ð	818
Bes	Similarity 18.1%; Pred. No. 0.00015; 1; Conservative 268; Mismatches 675; Indels	A	1541 QLRQQITEKE
à	MPDLSHL-TEEERKIILAVMDROKKEEKEOSVLKIKEHKAOP 6	ò	862 RSDKNRRTK
đ		요	1591 OKDELDVRIT
ò	YKROVKOMGRR	à	920 BILIE
Q Q		8	1637 KVPEQQRQIT
à		Š	966 PTRRLQRSKR
g		đ	1691 STPRASIRPM
à	LIKSGAMFYNSGSNTLQQPDQKVP-RGLRNEEAPQEKKAKLHBOPOFOG	ð	1026 PHRVDVIGRT
g	LKLSEVRLSOORB	අධ	1735 VEHVPVFGST
à		è	1078 YSSDRDRDCE
q		<u>අ</u>	1774
à	287 YEQSERRDYSQYVPSDGTMPRSPSDYADRRSQREPQFYEEPGHAYRD 335	ò	1128 PSLMTGRSAP
		9 0	1813 TAVFGTVSAT

336 336 916	ENEVEGRHTLTRNLDVOLLDTRRQILDTETNI-HLANTKELLKNAQKEI ATLKQHLSNMEVQV SNRRGHRHSKEYI VDDEDVEGEDEYERQREEEFYQARYRSDPNLARYPV
385	
426	
486 1091	
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558	SIABTREVAQVESLRYRQRVELLERSESVSEKGDSQKGTR
593	EQGVISDSNITRSERQKKRMYYGGHSIEEDLEWSEPQIKDSGVDTCSSTTIANEEHSHS 649
650	LQABKKGLEBDVKRWKARNGHLV
692 1367	
733	GRLILQGAMFREVYNIILRSKDEPGVELAVSRPIGDIPRIPDST 775
776	HAQLESSSSFESQRUDRPSISVTEPMSPGMLEDVPQFLSGQ 817
818	OLRQQITEKEEKTRKALVAAKSKIAHLAGVKDQLIKENEELKQRNGALDQ 1590
862	RSDKNKRITKTVKKTLEPKNNQTPIYSPVHRREFRERMLEITLMDQARVREESSFLG 919
920	EILIELETALLDDEPHWYKLQTHDVSSLPLFRPSPTLPRRQLHGES 965 ::
966 1691	
1026	PHRVDVIGETREWEBSAPPPORNVEGGHRGTRATGHYMTISRWDRHRVMDDH 1077
1078	YSSDRDRDCEAADROPYHRSRSTEQRPLLERTTTRSRSSERPDTNLARSM 1127
1128	PSIMTGRSAPPSPALSRSHPRTGSVQTSPSSTPGTGRRGRQLPQLPPKGTLERSA 1182 ::

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or send an email to license@isb-sib.ch).
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19.5%; Pred. No. 0.0002;
ative 204; Mismatches 636; Indels 53;
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MW; 3CBB2EA8A34E8F47 CRC64;
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PEan; PFF0051; Armadillo.seg; 4.
SMART; SMO0185; ARM; 5.
PROSITE; PSS0176; ARM ERPEAT; 1.
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                                         WARESTDGEVETOVY-----NQDSQDSIGEGVTQGDYTPMEDSERTS-QSLQIDL 1920
                                                                         1238 SDVSAVSRISSASRFSSISYMSVQSERPRGNRKISVFTSKMQNRQ--------MGVS 1286
                                                                                                                                       GKNLTKSTSISGDMCSLEKNDGSQSDTAVGALGTS-GKKRRSSIGAKMVALVGLSRKSRS 1345
        MDIBERNROMKLNKYKQVAGSDPRLEQDYHSKYRSG-----WDPHRGADTVSTKSSDSDV 1237
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=Spreague-Dawley, and Fischer 344/N;
MEDLINE=95148647; FubMed=7946077;
Kakiuchi H., Matanabe M., Oshijima T., Toyota M., Imai K.,
Weisburger J.H., Sugimura T., Nagao M.;
"Specific S'-GaGA-3' mutation of the Apc gene in rat colon tumors induced by 2-amino-1-methyl-6-phenylimidazo[4,5-b]pyridine.";
Proc. Natl. Acad. Sci. U.S.A. 921910-914(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FUNCTION: Tumor suppressor. Promotes rapid degradation of CTNNB1 and participates in Wht signaling. APC activity is correlated with its phosphorylation state (By similarity).
                                                                                                                                                           2018 ADSQNSGKGNTGAAESSFSQEVSREQQPSSASE-----ROAPR----APQSPRRPPHP
                                                                                                                                                                                                                                                                                                 2067 LPPRLTIHAPPQ-----BLGPPVQRIGMTRRGSVGRGIQLTPGIGGMQHFFDDEDR--
                                                                                                                                                                                                          ASQLSQTEGGGKKLRST----VQRSTETGLAVEMRNWMTRQASRESTDGSMNSYSSEGNL
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=Flecher 344/N; TISSUE=Brain; MEDLINE=96116966; PubMed=8563176; Toyoca M., Ushijima T., Kakiuchi H., Watanabe M., Imai K., Yachi A., Sugimura T., Nagao M.; "cDNA cloning of the rat APC gene and assignment to chromosome 18."; Mamm. Genome 6:746-748(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUBUNIT: Forms homooligomers. Associates with catenins. Binds axin (By similarity).
PTM: PHOSPHORYLATED BY GSK-3B (BY SIMILARITY).
SIMILARITY: Contains 7 ARM repeats.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-SBP-2003 (Rel. 42, Last amnotation update)
Adenomatous polyposis coli protein (APC protein)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
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1948 L.	Db 2766	Qy 1566	Db 2808	5 J	AC 061315; C DT 16-0CT-20		A Age	OS Mus muscu OC Eukaryota	OC Mammalia; OX NCBI_TaxI	RP SEQUENCE	RX MEDLINE=9 RA Su LK		, <u>,,</u>		Su LK.			RA DICKET F. RT "The muri	- to -		RA MEDULINES RA OShima M. RT "APC gene	RL Cancer Re			!	CC Iso			CC ISO	+	CC -1- SIMIL	CC This SWIS	CC use by
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SSKHSSPSGTVAARVTPFNYNPSPRKSSADSTSA------RPSQIPTP 2807
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M., Sugiyama H., Kitagawa K., Taketo M.;
An messenger KM: novel isoforms that lack exon 7.";
Ase. 53:5589-5591(1993).
TION: Tumor suppressor. Promotes rapid degradation of CTNNB1
participates in Wnt signaling. APC activity is correlated with
phosphorylation state (By similarity).
NIT: Forms homooligomers. Associates with catenins. Binds
1 (By similarity).
SENATIVE PRODUCTS:
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15.78L/61, and CAST/R1; TISSUR-Brain;
1-92263101; Pubmed=1350108;
1-9.78. Analar F. M., Vogelstein B., Preisinger A.C., Moser A.R.,
C., Gould K.A., Dove W.F.;
1e intestinal neoplasia caused by a mutation in the murine of the APC gene.";
256:668-670(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              . Kinzler K.W., Vogelstein B., Preisinger A.C., Moser A.R., C., Gould K.A., Dove W.F.;
256:1114-1114(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                a; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
1; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
:ID=10090;
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UR SPECIFICITY: EXPRESEED IN LIVER, SPLERN, KIDNEY, HEART,
FRAIN, STOMACH, UNTESTINE, TESTIS AND OVARY.
FROSEPHORYLAYED BY GSK-3B [BY SIMILARITY).
LARITY: Contains 7 ARM repeats.
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rine APC gene: alternative splicing of 5' untranslated
Begments.";
ad (OCT-1993) +0 +1-
                                                                                                                                                                                                                                                                                                                                                                    1001 (Rel. 40, Created)
1001 (Rel. 40, Last sequence update)
1003 (Rel. 42, Last annotation update)
1008 polyposis coli protein (APC protein) (mAPC).
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sold=Q61315-1; Sequence=Displayed;
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                                                                                                                                                                                    1643 EGTPINFSTATSLSDLTIRBPPNELATGDGVRAGIQSGBFERRDTIPTEGRSTD---DAQ 1699
                                                                                                                                                                                                                                                                                        :||
1700 RGKISSIVTPDLDDNKARRGDILARCINSAMPKGKSHKPFRVKKIMDQVQQASSTSSGAN 1759
                                                                                                                                                                                                                                                                                                                                          ::||:
1760 KNQVDTKKKKPISPVKPMPQNIEYRIRVRK----NIDSKVNVNIEBIPSDNKDSKRPSLQ 1815
                                                                                                                                                                                                                                                                                                                                                                                                                                              2089 HAPSPGSENFDWKAIQEGANSIVSSLHQAAAAACLS-----RQASSD--SDSILS 2137
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -SGSPHRVDVIGRTRSWSPSARPPORNVEQGHRGTRATGHYNTISRMDRH--RVMDDHYS 1079
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SDRDRDCEAADRQPYHRSRSTEORPILERTTTRSRSSERPDTNIARSNPSIATGRSAPPS 1139
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                                  1403 SVQSEPCSGMVSGIISPSDLPDSPGQTMPPSRSKTPPPPPPQTVQAKREVPKSKVPAAEKR
                                                                                        1463 ESGPKOTAVNAAVQRVQVLPDVDTLLHPATESTPDGPSCSSSLSALSLDEPFIQKDVELR
                                                                                                                                                                                                                                                                                                                          ----ERQKKRMYYGGHSLEEDLEWSEPQIKDSGVDTCSSTTLNEEHSHSD----KHPVTW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    833 VIILGAKDLPSREDGRPRNPYVKIYFLPDRSDKNKRR------TKTVKKTLEPKWN
                    ------DPNLARYPVK---POPYBROWRIHAEVSRAR---HERR
                                                                  441 RAAMENQRSYSMERTREAQGQSSYPQRTSNHSPPTPRRSPIPLDRPDM------
                                                                                                                                                                     ----RRADSLRKOHHLDPSSAVRKTKRBKMETML-RNDSLSSDQSRSVRP--PPPR----
                                                                                                                                                                                                                      ---PHKSKKGGKMRQVSLSSSERRLAS-----TPRYTSCDDVELRSRSVSRKGDSQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              85 LOPQOKOP---NEKEPOTKIHQOFEMYKEOVKKMGEESQOQQQQQGDAPTC---GICHKT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
3.1%; Score 254.5; DB 1; Length 2845;
Best Local Similarity 18.8%; Pred. No. 0.00021;
Matches 362; Conservative 241; Mismatches 692; Indels 633; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ---- FPFSGITELVNNV
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Missing (in isoform 2 and isoform 4).

/FILd=WSP 004116.

Missing (In isoform 3 and isoform 4).

/FILd=WSP 004117.

T -> A (IN STRAIN CAST/EI).

V -> I (IN STRAIN CAST/EI).

Y -> P (IN STRAIN CAST/EI).
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T -> A (IN STRAIN CAST/EI).

Y -> F (IN STRAIN CAST/EI).

A -> T (IN STRAIN CAST/EI).

A -> T (IN STRAIN CAST/EI).

G -> A (IN STRAIN CAST/EI).

H -> Q (IN STRAIN CAST/EI).

T -> A (IN STRAIN CAST/EI).

T -> A (IN STRAIN CAST/EI).

T -> A (IN STRAIN CAST/EI).

T -> S (IN STRAIN CAST/EI).

M; 145CA73CF570A499 CRC64;
                                                                                    GO; GO: 0005737; C: Cytoplasm; IDA.
GO; GO: 0005634; C: nucleus; IDA.
GO; GO: 0005634; C: nucleus; IDA.
GO; GO: 0008613; F: Deta-catenin binding activity; IDA.
GO; GO: 0016055; P: Wht raceptor signaling pathway; IDA.
INTERFO; IRR000225; Armadillo.
Pfam; PF00514; Armadillo. seg; 4.
SWART; SW00185; ARW, 5.
Wht signaling pathway; Anti-oncogene; Phosphorylation;
Alternative splicing; Repeat; Coiled coil.
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ARM 6.
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ASP/GLU-RICH (ACIDIC).
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email to license@isb-sib.ch)
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K-LNKYKO : KGLNQMSN	SRFS IKEAPSPT	GD	MVAIVGLS : LPRVSTWR	SDISPTGM	PGVR : GNTPPVID	ARGLVVKF : QKGTEAKP	LQIIVWGD : AARVTPFN	SSLESSTG : : : TDITESSG
2399	1250	1298	1333	1380	1404	1458	1517	1577
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Search completed: December 12, 2003, 07:15:04 Job time : 62 secs

- protein search, using sw model OM protein Run on:

December 12, 2003, 06:26:30 ; Search time 49 Seconds (without alignments) 3120.576 Million cell updates/sec

Perfect score:

US-09-617-099B-1 8285 1 MSAPIGPRGRPAPTPAASQP.....TRRASQSSLESSTGPSYSRS 1590 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283308 segs, 96168682 residues Searched:

283308 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

PIR 76:*
!: pir1:*
!: pir2:*
!: pir3:*
!: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

hypothetical prote hypothetical prote hypothetical prote hypothetical prote hypothetical prote hypothetical prote trichohyalin hume hypothetical prote rabphilin-3A - mou rabphilin-3A - rat rabphilin-3A - bov rab3 effector prot profilaggrin relat microtubule-associ proliferation pote Description T20531 JX0338 I58166 A48097 129736 100332 100332 125753 134318 84644 A45973 149316 113564 T03301 80 Query Match Length 547 1021 1898 1386 1386 1560 2526 681 704 1002 500.5 475.5 437 Score Result ģ

יהיספספ בים (ייולנידים ויות	protein F07A11 6 [microtubule-associ	hypothetical prote	Cell proliferation	Muncl3-3 protein -	trichohvalin - rab	hypotherical prote	hypothetical prote	·c	sericiniB - gilken	DNA-binding protei	~	_	_		
A37981	E88320	313507	T00037	T30249	42759	828589	729253	T16270	860254	352714	T42717	T34036	F19823	113592	126135	
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1830	2738	1825	1323	2938	2207	1407	1558	1827	2453	1217	2282	1359	1695	1306	1829	
2.9	6.	2.8	2.8	2.8	2.8	9. 8	2.8	2.8	2.8	2.8	2.7	2.7	2.7	2.7	2.7	
236.5	236.5	236	234.5	234.5	234	233.5	232.5	231	230.5	228	227.5	227	227	225.5	225.5	
30	31	32	33	34	35	36	37	38	33	40	41	42	43	44	45	

ALIGNMENTS

rab3 effector protein Rim - rat C;Species: Rattus norvegicus (Norway rat) C;Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 08-Oct-1999 C;Accession: T03301

Riwang, Y.; Okamoto, M.; Schmitz, F.; Hofmann, K.; Sudhof, T.C.
Nature 388, 593-598, 1997
A; Title: Rim is a putative Rabl effector in regulating synaptic-vesicle fusion.
A; Reference number: Z14897; MUID:97394473; PMID:9252191
A; Reference number: T03301
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Residues: 1-1553 «MAN.
A; Residues: 1-1553 «MAN.
A; Cross-references: EMBL:AF007836; NID:92317777; PIDN:AAB66703.1; PID:92317778
A; Reperimental source: tissue-type brain

C, Genetics:

A;Description: Rim protein is proposed as Rab3-dependent regulator of synaptic-vesicle C;Reywords: GTP binding; zinc finger

37; Query Match

54.2%; Score 4489.5; DB 2; Length 1553;
Best Local Similarity 57.2%; Pred. No. 4.2e-214;
Matches 952; Conservative 209; Mismatches 319; Indels 183; Gaps à

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61 KEEHKAQP-----TQNFPFSGITELVNNVLQPQQKQPNEKEPQT--KLHQQFEMYKE

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111 QVKKONGERSQQQQ-BQKGDAPTCGICHKTKPADGCGHNCSYCQTKPCARCGGRVSLRSNK 169 116 57 VVRDMAKPAACKTPRNAESQPHQPPLNIFRCVCVPRKPSSEEGGPERDMKLHQQFESYKE ద ò

218 170 ----VMWYCNLCRKQQEILTKSGAWFYNSGSNTLQQPDQKVPRGLRNE-----RAPQE 윱 Š

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protein hypothetical

OY 1428 GROTLATPAMGDIGVGMM Db 1391 GROTLATPAMGDIGVGME CY 1488 KKKTVARKTLEPLYQQL Db 1451 KKKTRIARTLDPLYQQS OY 1548 NAVIGWFKLPPPSSLVDP DD 1511 SMVIGWFKLPPPSSLVDP	RESULT 2 T29736 hypothetical protein T10A3.1 - C C;Species: Cemorthabditis elegan C;Bate: 15-Oct-1999 #sequence_re C;Accession: T29736 R;Sansone, J.; Nhan, M. submitted to the ERRIL Data Libra: A;Description: The SRGIL Data Libra: A;Reference number: Z20675 A;Reference number: Z20675 A;Accession: T29736 A;Accession: T29736 A;Accession: T29736 A;Koperimental Prope: DNA A;Residues: 1-853 - CSAN> A;Residues: 1-853 - CSAN> A;Residues: 1-853 - CSAN> A;Residues: 1-853 - CSAN> A;Residues: CSEP:T10A3.1 A;Map position: X A;Introns: 41/3; 110/1; 151/2; 1:	Query Match 12.1%; Best Local Similarity 29.7%; Matches 300; Conservative 1.	Db 215 NWTLTSRNRSTSSYYYSD Db 215 NWTLTSRNRSTSSYYYSD Oy 834 TILGAKDLPSREDGRPRW :
334 ERRETRRIEKGRSQDYSDRPEKRDNGRVAEDQKQRKEEEYQTRYRSDP 381 378 NLARYPVKPQFYEEQMRIHAEVSRARHERRHSDVSLANAELEDSRISLLEMDRPSRQRSV 437		856 IYPLPDRSDKNKRRTXCYKTLEPKWNOTPIYSPYHREFRERALETITUMOARVREEES 915 1	1037 LFRAKRGRSESLHMTSELQPSELDRARSASTNCILRPDTSILISPERERHSKESERCSIGKQ 1096 1133 GRSAPPSPALSRSHPRTGSESTPGTGRRGRCDLPRF-GTLERSAMDIEERNRQ 1911 1097 SRKGTASDA-DRTHRQGSPTQSPPADTSFGSRRGCLPQUPPR-GTLERSAMDIEERNRQ 1151 1192 MKLNKYKQVAGSDPRLEQDYHSKYRSGMPDRQLPQVPRGSIEQASLVVBERRTRQ 1155 1195 MKLNKYKQVAGSDPRLEQDYHSKYRSGMPDRGADTVSTKSSDSDVSDVSAVSRTS 1247 1196 MKLNKYKQVAGSDPRLEQDYHSKYRSGMPDRGADTVSTKSSDSDVSDVSAVSRTS 1247 1196 MKLNKYKQVAGSDPRLEQDYSKYNIHRDQYRSCDNASAKSSDSDVSDVSAVSRTS 1247 1196 MKLNKYKQVAGSDPRLEQDYSKYNIHRDQYRSCDNASAKSSDSDVSDVSAVSRTS 1247 1196 MKLNKYKARRGYSTSTRRRKISVFTSKMQNRQMRWGTSGRALTKSTSSGMPGSLEKND 1307 1197 GSQSDTAVGALGTSGAKRARSTSGARGATKKAKSTTQRST 1307 1198 GSQSDTAVGAGAKRRSSLGAKWALVSRRSRSTSQLSQTESGGRKKAKSTTQRST 1317 1318 ETGLAVERNWMTRQASRESTDGSMNSYSSEGNLIFPGVRLASDSQFSDFLDGLGPAQLV 1427 1318 ETGLAVERNWMTRQASRESTDGSMNSYSSEGNLIFPGVRLASDSQFSDFLDGLGPAQLV 1427 1318 ETGLAVERNWMTRQASRESTDGSMNSYSSEGNLIFPGVRVQFDSQFSDFLDGLGPAQLV 1427 1318 ETGLAVERNAMMTRQASRESTDGSNNSYSSEGNLIFPGVRVQFDSQFSDFLDGLGPAQLV 1427 1318 ETGLAVERNAMMTRQASRESTDGSNNSYSSEGNLIFPGVRVQFDSQFSDFLDGLGPAQLV 1390 1318 ETGLAVERNAMMTRQASRESTDGSNNSYSSEGNLIFPGVRVQFDSQFSDFLDGLGPAQLV 1390 1319 H
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194/1; 232/1; 342/3; 390/3; 528/1; 551/2; 628/1; 674/2;
                                                                36;
MOKKGOLEVELIRARGLVVKPGSKTLPAPYVKVYLLDNGVCIA 1487
                   PTRRLORSKRISDSKVSDYDCEDGVGVVSDYRHNGRDLQSSTL 1008
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PHRVDVIGRIRSWSPSAPPPORNVBQGHRGTRATGHYNTISRM 1068
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LEWNGRLLOGATFEEVYNIILESKPEPQVELVVSR----PIGD 767
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ----SSFESO---KMDRPSI-----SVTSPMSPGML--- 807
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SRVPSAYPSQPQRQLPNPDLFLDIHPALQQLSLPHSQSAVFPH 214
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NPYVKIYFLPDRSDKNKRRTKTVKKTLSPKNKGTFIYSPVHRR 893
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REERSEFICEILIELETALLIDBEPHWYKLQTHDVSSL--PLPR 951
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; FIDN:AAB37028.1; GSPDB:GN00028; CESP:T10A3.1 iristol N2; clone T10A3
                                                                                                                                                                                                                                                                                     evision 15-Oct-1999 #text_change 18-Feb-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;; Score 1002; DB 2; Length 853;
;; Pred. No. 4.8e-42;
142; Mismatches 252; Indels 316; Gaps
                                                                                                                                PTSAPLTRRAGOSSLESSTOPSYSRS 1590
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C. elegans cosmid T10A3.
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### ### ### ### #### #### ############	QY 1280 NRQWGSGRALTKSTSISGIMCSLERANGSQSDTAAVGALGTSGRACRSS	RESULT 4 T00332 hypothetical protein KIAA0559 - human (fragment) C;Species applens (man) C;Species Rome applens (man) C;Accession: T00332 R;Nagase, T.; Ishikawa, K.; Miyajima, N.; Tanaka, A.; Kotani, H.; Nomura, N.; Ohara, C R;Nagase, T.; Ishikawa, K.; Miyajima, N.; Tanaka, A.; Kotani, H.; Nomura, N.; Ohara, C DNA Res. 5, 31-39, 1998 A;Title: Prediction of the coding sequences of unidentified human genes. IX. The compl A;Reference number: Z14086; MUID:98296545; PMID:9628581 A;Reference number: Z14086; MUID:98296545; PMID:9628581 A;Reference number: Z14086; MUID:98296541; PIDN:BAA25485.1; PID:93043642 A;Residues: 1-1212 cNAG> A;Residues: 1-1212 cNAG> A;Residues: L-1212 cNAG> A;Residues: L-1212 cNAG> A;Roberimental source: Drain C;Genetics: A;Note: KIAA0555 C;Superfamily: protein kinase C C2 region homology F;965-1088/Domain: protein kinase C C2 region homology
421DHISQNIDKQPHHHHLAPNDBENDEYIDDDELENDI 1129 SIMTGRSAPPSPALSRSHPRTGSVQTSPSSTPGTGRRGR	Db 725 IIRAKNLVVRPGVKLTFSAFYVKVYLARGKQCIAKAKTNAATKTTSFLFQQHLIFNDSFK 784 QY 1514 GRVLQITVMGDYGRAMDHKSFMGVAQILLDBLEL-SNAVIGWFKLFPSSL 1562 Db 785 KRTLQVTVLGDYGRWERKVFWGISQIRLEDLELGSQPLIGWYKLFPSSL 1562 TO0634 TO0834 TO083	A; hintrons 36/2, 59/1, 130/3; 172/2; 203/3; 227/3; 288/1; 353/1; 414/1; 461/2; 486/1; 55 A; Note: H_D0897G10.1 C; Superfamily: protein kinase C C2 region homology CKC2> C; Superfamily: protein kinase C C2 region homology CKC2> Query Match

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980 EVSDYDCEDGVGVVSDYRHINGRDLQSSTLSVPEQVMSSNHCSPSGSPHRVDVIGRTRSWS 1039
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                                                       316 RRSQREPOFYEEPGHLNYRDSNRRGHRHSKEYIVDDEDVESRDEYE----RQRREEBYQ- 370
                                                                            | | : | : : | : | : | CTESLDHLAGLSHYYHADTSYRHPPKSEKYSISRLTLEKQAAKQLPAALLYQKQSKHKKS 471
                                                                                                                                                                                        530 OKFMGSSLGTGLGTLGNTIRSALQDBADKPYSBGSRSRPSSRPSSVYGLDL-----SI 582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DKNKRRTKTVKKTLEPKWNQTFIYSPVHRREFRERMLEITLWDGARVREEESEFLGEILI 923
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EL-ETALLDDEPHWYKL--QTHDVSSLPLPRPSPYLPRRQLHGES-PTRRLQRSKRISDS 979
                                                                                                               -------SRARHERR 407
                                                                                                                                                                        HSDVSLAN-AELEDSRISLIRMDRPSRQRS-----VSERRAAMENQRSYSMERT---- 455
                                                                                                                                                                                                                                 ------PLDRPDWRRADSL 494
                                                                                                                                                                                                                                                                                      RKOHHLDPSSAVRKTKREKMETMLRNDSLSSDQSESVRPPPPRPHKSKKGGKMRQVSLSS 554
                                                                                                                                                                                                                                                                                                                                               SERBIAS-------TPEYTSCDDVELESESVSEKGDSOKGKRKT----- 591
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                                                                                                                                                                                                                                                                                                                                                                                                                                 696 AFIMDDFOHAMSDSEAY-----HIRRERTDW------POKPRESRIENGH 734
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5.7%; Score 475.5; DB 2; Length 1212;
llarity 23.3%; Pred. No. 8e-16;
Conservative 137; Mismatches 297; Indels 267;
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|PSRSQSKTSVTQTH 1185
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             Best Local Similarity
Matches 213; Conserv
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T25753 hypothetical protein P45B4.3 - Caenorhabditis elegans

RESULT 5

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429
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ----TYLHQQFEMYKEQVXXMGEESQQQQEQKGDAPTCGICHKTKPADGCGHNCSYCQTK 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               215 APQEKKAKLHBQPQFQGAPGDLSVPAVEKGRAHGLTRQDTIKRGSGVKHQIASDMPSDRK 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         275 RSPSVSRDONRRYEQSEEREDYSQYVPSDGTMPR-----SPSDYAD--RRSQREPQFYE 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              504 LNPNVPMS-----SDYSSHVPHYGSLPRIDYPRGTRSDVRDFTYROCHLPCOPP 552
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              612
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    471 HSPPT----PRRSPIPLDRPDMRRADSLRKQHHLDPSSAVRKTKREKMETWLKNDSLSSD 526
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                                                   A;Gene: CSSP:F4584.3
A;Map position: 4
A;Introns: 25/3; 859/1; 928/1; 966/1; 1002/2; 1106/2; 1167/1; 1255/1; 1274/2
                 C/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999 C/Accession: 725753
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    375 KRSAETÇIR----LANYESITPIVRYGSIPRSSRERTABRRYREÇÇÇIYNÇMPÇNHND
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                                                                                                                                                                                                                                                                                                                                           Query Match 5.3%; Score 437; DB 2; Length 1325;
Best Local Similarity 20.2%; Pred. No. 7.2e-14;
Matches 242; Conservative 151; Mismatches 405; Indels 400; Gaps
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262 SQUADANQINGANGRICALINTEDENERGY INDDEDVESRDETERGREEFYGARTR - SDPHLARY 382 262 SQUADANQINGANGNON 262 SQUADANQINGANGNON 263 264	RESULT 7 844644 hypothetical protein F37A4.7 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 24-Sep-1999 C;Accession: 844644; T16287 R;Pulton, L. R;Pulton, L. R;Pulton, L. R;Pulton, L. R;Pulton, L. R;Pulton, L. R;Pulton, L. R;Pulton, L. R;Pulton, L. R;Pulton, L. R;Pulton, L. R;Pulton, L. R;Pulton, L. R;Pulton, L. R;Pulton, E. R;Rerence number: 844638 A;Recession: 844644 A;Residues: 1-1021 <full 1-1021="" 101="" 153="" 198="" 1;="" 234="" 2;="" 344="" 3;="" 462="" 519="" 592="" 616="" 74="" 741="" <full="" a;gene:="" a;introns:="" bomology="" bristol="" c="" c2="" c3="" c;genetics:="" c;superfamily:="" cesp:f37a-a;residues:="" crsp:p37a4.7="" domain:="" embl:u00032;="" f;76-991="" homology="" kcc2a-a-a-a-a-a-a-a-a-a-a-a-a-a-a-a-a-a-a<="" kinase="" n2="" nid:9458958;="" pid:9458965;="" pidn:aaa50635.1;="" protein="" r;76-991="" r;cross-references:="" r;experimental="" region="" source:="" strain="" th=""><th>LEGAL TO THE TANK THE</th></full>	LEGAL TO THE TANK THE
Colorador Colo	014 VMSSNHCSPSGSPHRVDVIGRTRSWSPSA 205 AAASKHSAAVHNHH	Similarity 23.0%; Pred. No. 1.9e-10; O; Conservative 99; Mismatches 225, TEEERATILAVMDROKKEERERGOSULKIKEEHKAOPTOW

19 OPPPOPEMPDLSHLTEERRKIILAVMOROKKEERKBOSVLKIKERHRAOPTOMPPFSG 76	BPORORELOBEBEQLARIERQEI-RRERGEEGOOGRIERERGEE	OKOPNEKEPOTKLHOOFEMYKEGYKUMGERSOOOGEOKGDAPTCG		ICHKTKFADGCGHNCSYCQTKFCARCGGRVSLRSNKVMWVCN	REGOL	194 SGSNITLQQPDQXVPRQLANEKAPQBXXAX.HISQPQPQGAPGDLSVPAVEKGRAHGLTRQD 253 1	TIKMGSGVKHQ1ASDMPSDRKRSPSVSRDQNRRYEQSEKR-EDYSQYVPSDGTMPRSPSD	413 QLRREQQLRREQQLRREQQLRREQQLRREQQLRREQGRREGGRREG	313 YADRREQREPOFYEEFGHLNYRDSNRRGHRHSKRYIVDDEDVE 355	rkönlkreesterhegeräkkoolkrdoeberrernikleeberärreoolregoe	356 SRDE-YERORREGYOARYESDPYIARYPUKPOPYEGORITHAKYSRARHERHSDVSLA 414		587 KREQEERRUOLIKREBERROOLIKREGEERLEGR-IKREEVERLEGEERRUERLEREF 645	475 TPRRSPIPLDRPDMRRADSLRKQHHLDPSSAVRKTKREKMETMLRNDSLSSDQSESVRPP 534	BERRHELLKSERGEERRHEQLRREGOE	535 PPRPHKSKKGGKWRQVSLSSSERELASTPRYTSCDDVELSSBVSEKDSGKGK 588	-RKTSEÇGVLSDSNITRSERQKKRMYYGGHSLEKDLEWSEPQIKDSGVDTCSSTILNEKHS	738 VILLRAPQAGRARARAPQEQERKRRR	648 HSDKHPVTWQPSKDGDRLIGRILLANKRLKDGSVPRDSGAMLGLKVVGGKWTESG 701	773 HRQQQBBBQRDFTWQWQABEKSBRGRQRLSARPPLRBQRBRQLRABBRQQRBQR 827	RICAFITKVKKGSLADTVGHLRPGDEVLEWNGRLLQGATFREVYNIILESKPERPVBLVV	FL	76Z SKFIGDIFKI PUSTRAQUESSUSSEFESQAMUSPESISVI SFESSFESGAMUSPESIS 821	WIND KYCHOLI VIII GAKOLIPSREDGRENDYNYMY Y TYPORSOKWYRYTYKYTI RPIK	KWRWQL	882 NOTFIYSPVHRREPRERMLBITLMDQARVRBERSEFIGEILIELETALLDDEPHMY 937	932 REEREKRRRQEGERQYREKERQLQQSERQLLREEREKRRRQERERQYRKUK 981	KLOTHDVSSLPLPRPSPYLPRQLHGESPTRRLQRSKRISDSEVSDYDCEDGVGVVSD	98Z KLÓOKE		
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DD 393 NMERFSKHTHAHANRLYSTDDDDGSPESRRSTRSTG	QMRIHAEVSRARHERRHSDVSLANAELEDSRISLLRMDRPSRQRSVSERRAAMENQRSYS	Db 435GITCS 478	452 MERTRRAQQOSSYPQRTSNHS-PPTFRRSPIPLDRPDMRRADSLRKQHHLDPSSAVRKTK	479 SSSLTPLQQQASHDHHSGGGTPRRISNPDRTTS	511 REKMETMLRNDSLASDQSESVRPPPRPHKSKKGGRMRQVSLSSSEEELASTPEYTSCDD	DD 512 RV5QSASGTSLYTPPPPISSRTSPDNCNSSPLNV 545 OV 571 VELKSRSVSRKGDSOKGKRKT-SROGVLSDAWFRSRROWKRNVYGHSLREDI 629	546MEHKSSSASTASSGGNRRVGSAEPVLNNHHAMHNNQNHNDINKKLISQTSR	Qy 630 KDSGVDTCSSTTLNBEHSDKHPVTWQPSKDGDRLIGKILLANKRLADGSVPRDSGAMLG 689	Db 597 AESPLAASSFLSSPDDDTKQKNRREDGVGRVNSLQLRTSLDDVAPP 643	690 LKVVGGKMTESGRLCAFITKVKKGSLADTVGHLRPGDEVLEMNGRLLQGATFEEVYNIIL	Db 644IVAPISRANGHGHIV 655 Qy 750 ESKREPQVELVVSRPIGDIPRIPDSTHAQLESSSSFRSQRANDRPSISVTSPMSP 804	DD 656 SSEPTSSTTSNQNHTSVPIPTVPVVPERBEREKAITASTESASEPGAVIRPLLLDIDENLEP 715	LRDVPQFLSGQLSIKLMFDKVGHQLIVTILGA	Db 716 KHASRRRGDGVRGVPRCLLCPSRKQRSLGSITLTLTYHSADKKLKAMLLRAKNLKAMDSN 775	848 RPRNPYVKIYFLPDRSDKNKRRTKTVKKTLRPKWNOTFIYSPVHRREFRERMLEITLMDO	DD 776 GRSDPYVKFHLLPGNTKATKLTSKTIEKTLNPEWNEEMSYGITEDDKEKKLLKVTVLDR 835 CV 908 ARVRERESFEIGRILIELETATLDBEPHWYKLOTHDVSSLDLDR 941	836 DRIGSDFLGETRIALK-KLNDNEMKKFNLYLRSALPVPQ		KESULI B FULL STATE STA	cricinosysism - muman C;Species: Homo sapiens (man) C:Date: 03-May-1994 #semmence revision 01-May-1996 #text change 22-inn-1999	DV, L.N.; O'Keefe, B.J.; Parry, D.A	J. BIOJ. CAGMI. 256, 12164-12176, 1993 A. Title: The structure of human trichohyalin. Potential multiple roles as a functional E	eu (cross-linking) procein. A;Reference number: A45973; MUID:93280194; PMID:7685034 A;Accession: A45973	A; Molecule type: DNA A; Residues: 1-1898 < LEE>	erences: GB:L09190; NID:g292835; PIDN:AAA65582.1; PID:g292836 hors translated the codon AGG for residue 1714 as Pro	CyComment: Trichonyain is a protein of the medulia of the hair and of the inner root sprovalent modifications to this protein include conversion of arginine to citrulline and	Sychotics: A;Gross-references: GDB:136223: OMIM:190370	Map position: 1q21-1q21 Superfamily: trichohyalin; calmodulin repeat homology	C;Keywords: calcium binding; citruline; EF hand; hair; tandem repeat F;49-81/Domain: calmodulin repeat homology <bf2></bf2>	Query Match 3.7%; Score 307; DB 1; Length 1898; Best Local Similarity 17.4%; Pred. No. 3e-07; Matches 245; Conservative 213; Mismatches 514; Indels 434; Gaps 53;	

417 ELEDSRISLLRMDRPSRQRGVSERRAAMENGRSTSMERTREAGGQSSYPQRTSN 470 11	471 HSPPTPRRSPIPLDRFDMRRADSLRKQHHLDPSSAVRKTKREK	515 STMLRNDSLSSDQSESVRPPPPRPHKSKKG-GKWRQVSLSSSERELASTPRYTSC		624WSEPQIKDSGVDTCSSTTLAREHSHSDKHPVTMQPSKOGDR	665 LIGRILLMKRLKDGGVPRDSGAMLGLKVVGGKATEBGRLCAFITKVKKGSLADTVGH	722IRPGDEVLEMNGRLLQGATFEEVYNIILESKFERQVELVVSRPIGDIPRIPDST 775	776 HAQLESSSSSFESQNWDRPSISVTSPWSDGMLRDVP 81.1	812 OFLSGQLSIKLMFDKVGHQLIVTILGAKDLPSRE-DGRPRNPYVKIYFLPDR 862	863SDKNKRTKTVKKTLEPKNNQTFIYSPVHRRFRERMLEITLMDQARVRERE 914	915 SEFICELIELERTALLDDEPHWYKLQTHDVSSLPLPRPSPYLPRRQLHGESPTRRLQ- 971	972	1031	1091 RQPYHRSRSTEQRPILERTTTRSRSSERPDTNIARSMPSIATGRSAPPS-PA 1141 1004 IBWYEHSPAPAPAVQAPRPAPPPFPFFISPGRGRQRQQQQQQQQQQQAAAPRQPPAAQPP 1063	1142 LSRSHPRIGSVQTSPSSTPGTGRRGRQLPQLPPKGTLERSAMDIEER 1188 1064 LIKPTSTLENSPVIRSGVSLRGYGRRKSLPPPIPPSNRNIVTPLQPLYPSLPPYSSF 1120	1189 NRQMIGLNKYKQVAGSDPRLEQDYHSKYRSGWDPHRG-ADTVSTKSBDBDVSDVSRTS 1247	1248 SASRFSSTSINGVQSRPRGHRKISVFTSRMCNRQMG 1284	RESULT 10 T13564 microtubule-associated protein homolog - fruit fly (Drosophila melanogaster) N;Alternate names: hypothetical protein EG:49E4.1
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CY 1053 HRGTRATGHYNTISRMDRHRVMDDHYSSDRDRDCBAADRQPYHRSRSTEGRFILERTTTR 1112	QY 1113 SRSSERPDTNIARSMPSLATGRSAPPSPALSRSHPRTGGVQTSPSSTPGTGRRGRQLPQL 1172 ::	OY 1173 PPKGTLERSAMDIEERNROMFLNKYKQVAGSDPRLEQDYHSKYRSGWDPH 1222 DD 1148 RRRQELERQYREEEELGROKRKGRYRDEDQRSDLKWGMEPEREKRAVRDNKV 1198	OY 1223RGADIVSTKS-SDSDVSDVSAVSRTSSASRFSSTSYMSVQSERFRGNRKIGVFTSKMQ 1279 1199 YCKGRENEQFRQLEDSGVRDRQSQQDLQHLLGEQQERDR	CY 1280 NRCMGVSGKNLTKSTSISGDMCSLEKNDGSQSDTAVGALGTSGKKRRSSIGAKNYAIVGL 1339 Db 1241 RRRWQQANRHFPEEEQLEREBGXEAKRR1268	QY 1340 SRKSRSASQLSQTRGGGKTLRSTVQR 1365 Db 1269 DRKSQSEKQLLRBEREBKRRRQFTDR 1294	RESULT 9 T49316 profilaggrin related protein [imported] - Neurospora crassa (fragment)	N;Alternate names: protein B13N20.10 C;Species: Neurospora crassa C;Anceseim: 02-0un-2000 #sequence_revision 02-Jun-2000 #text_change 02-Jun-2000	Rischulte, U.; Aign, V.; Hoheisel, J.; Brandt, P.; Fartmann, B.; Holland, R.; Nyakatura submitted to the Protein Sequence Database, May 2000 A;Reference number: Z25022 A;Acceseion: 149316	A;Status: preliminary A;Molecule type: DNA A;Residues: 1-1386 <26H>	A;Experimental source: BAC clone B13N20; strain OR74A C;Genetics: A;Gene: NCSP:B13N20.10 A;Map position: 6	Query Match 3.4%; Score 278.5; DB 2; Length 1386; Best Local Similarity 20.7%; Pred. No. 5.2e-06; Matches 284; Conservative 163; Mismatches 540; Indels 385; Gaps 62;	TYTLHQQPEMYKEQVKAMGEESQQQQEQKGDAPTCGICHKTKPADGCGHNC 1				ESRD : EVREVTEE	OY 359EYBRORREBEYQARYRSDPNLARYPVKPOPYEBOMRIHAEVSRARHERRHSDVSLANA 416

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ENOE-----DIMEOVKOKERHEO-----KIESGI---ITEKEAKKSASTP 1307
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     533 PP----PPRPH-----KSKKGGKMRQVSLSSSEEELASTPE--YTSCDDVELES-- 575
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C;Species: Drosophila melanogaster
C;Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 17-Nov-2000
C;Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 17-Nov-2000
C;Accession: 173564
A;Description: Sequencing the distal X chromosome of Drosophila melanogaster.
A;Reference number: 217689
A;Accession: T13564
A;Accession: T13564
A;Residues: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-5327 cSPA>
A;Cross-references: EMBL:AL031128; PIDN:CAA20006.1
C;Genetics:
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A,Introms: 24/2; 52/3; 104/3; 179/1; 232/1; 1669/3; 2566/1; 4798/3; 5272/1
A,Note: BG:4984.1
C;Superfamily: Drosophila 576K microtubule-associated protein homolog
                                                                                                                                                                                                                                                                                                                                          Gaps
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R;Witte, M.M.; Scott, R.E.
submitted to the EWEL Data Library, November 1998
A;Reference number: Z22246
A;Accession: T42727
A;Status: preliminary; translated from GB/EMEL/DDBJ
A;Molecule type: mRNA
                                                                                                                                                                              A; Description: involved in hnRNP association C; Superfamily: RING finger homology <R;57-107/Domain: RING finger homology <RRN>
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277 PSVSEDCRRAYEGGEREDYSGTVFSDTMFRBS-DTADREGGEPOFTERFORD 331 1 1 1 1 1 1 1 1 1	Cidente: 21-Jan-1994 #sequence_revision 18-Nov-1994 #text_change 05-Nov-1999 Cidente: 21-Jan-1994 #sequence_revision 18-Nov-1994 #text_change 05-Nov-1999 Cidente: 21-Jan-1994 #sequence_revision 18-Nov-1994 #text_change 05-Nov-1999 Cidentesion: A48097 #sequence_revision: A80097 #sequence_revision: A201-2068, 1993 A; Title: Rabphilin-3A, a putative target protein for smg p25A/rab3A p25 small GTP-bin A; Reference number: A48097; MUID:93204952; PMID:8384302 A; Reference number: A48097; MUID:93204952; PMID:8384302 A; Residues: 1-704 -8HI-A; Residues: 1-705
475 TPRESPIPIDREDMERADSIREQUALIDRESAVERTEREMETHARDESSD-QEESVRE 333	Query Match 3.2%; Score 262.5; DB 2; Length 684; Best Local Similarity 18.8%; Pred. No. 1.3e-05; Matches 177; Conservative 105; Mismatches 298; Indels 363; Gaps 38; Qy 42 AVMDROKKEBEKEQSVLKIKERHKAQPTQMFPFSGITELVNNVLQPQQK-QPNEKEPQTK 100 Db 35 AQTDQFRWYREQVKRAGEE

KBOSVLKI KERHKAQPTOWFPFSGITELVNNVLQPQCKQPNBKBPQTKLHQQ	FRETERGYKKWGEESQQQQEQ-KGDAPT-CGICHKIKFAUGCGHWCSICUTKFCKKCG 150 	GRVSLRSNKVMWVCNLCRKQQEILTKSGAMFYNSGSNTLQQPDQKVPRGLRNERAPQEKK 220	AKLHEQPQPQGAPGDLSVPAVEKGRAHGLTRQDTIKNGSGVKHQIASDMPSDRKR 275	SPSVSRDQNRRYEGSEEREDYSQYVPSDGTMPRSPSDYADRRSGREPGFYEEPGHLNYRD 335	SNRRGHRHSKEYIVDDEDVESRDEYERQRREBEYQARYRSDPNLARYPVKPQPYEBQMRI 395	Haevsrarherrhsdvslanaeledsrisllrmdrpsrorsvserraamenorsyswert 455		REAQGQSSYPQRTSNHSPPTPRRSPIPLDRPDMRRADSLRKQHHLDPSSAVRKTKREKWR 515	TMLRNDSLSSDQSBGVRPPPPRPHKBKKGGKWRQVSLSSS 555 : : :	BEBLASTPRYTSCDDVELBSBSVSRKGDSQKGKRKTSBQGV 596	LSDSWIRSERQKKRWYRGGHSLEBDLEWSEPQIKDSGVDTCSSTTLNEEHSHSDKHPVTW 656	QPSKDGDRLIGRILLANKRLKDGSVPRDSGAMLGLKVVGGKOTTESGRLCAPITKVKKGSLA 716	DIVGHLRRGDEVLEWNGRLLGGATFEEVYNIILESKPEPQVELVVSRPIGDIPRIPDSTH 776	AQLESSSSSFRSQKWDRPSISVTSPMSPGMLRDVPQFLSGQLSIKLWFDKVGHQLIVTIL 836		GAKULPSKEDGKFKKRIYKLIFLPDKSDKAKKIKIYKKILLFFKRANGFFISFYRKAFK 970 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : CVHILARDE NUGYSDP NUGWSTAR NUGWST	ERMLEITLWDGARVREBESEFLGBILIELETALLDDEPHWYK 938 :: - - - - - - - - - - - -
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Search completed: December 12, 2003, 07:20:58 Job time : 67 secs

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December 12, 2003, 07:16:45; Search time 609 Seconds (without alignments) 485.573 Million cell updates/sec
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1 MSAPLGPRGRPAPTPAASQP.....TRRASQSSLESSTGPSYSRS 1590
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	Sequence 1, Appli	Sequence 423, App	Sequence 449, App	Sequence 34248, A	Sequence 492, App	Sequence 2, Appli	+	Н	Sequence 32, Appl	Sequence 30, Appl	Sequence 30, Appl	~	Sequence 38199, A	Sequence 236, App
SUMMARIES ID	US-10-180-326-1	US-10-177-293-423	US-10-177-293-449	US-09-864-761-34248	US-10-339-782-492	US-10-144-198-2	US-10-144-198-4	US-09-987-482-1	US-08-681-219-32	US-10-092-138-30	US-09-230-111C-30	US-10-311-626-5	US-09-864-761-38199	US-10-341-434-236
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% Query Match	100.0	3.4	3.4	3.3	3.5	3.1	3.1	3.1	3.1	3.1	3.1	3.0	3.0	3.0
Score	8285	279	278.5	270.5	267.5	258.5	258.5	258.5	257.5	257.5	257.5	252	251	251
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Sequence 30, Appl Sequence 7, Appli Sequence 7, Appli Sequence 83, Appl Sequence 17, Appl	Sequence 470, App Sequence 4, Appli Sequence 12, Appli Sequence 2, Appli Sequence 4, Appli Sequence 95, Appli	m	HHH488	Sequence 1, Appli Sequence 2, Appli Sequence 8, Appli Sequence 2, Appli Sequence 2, Appli Sequence 224, Appli Sequence 224, App
US-10-094-466-30 US-09-764-176-7 US-09-824-574-7 US-10-171-311-83 US-10-287-218-17	US-10-153-668-470 US-09-902-422-4 US-10-144-198-12 US-11-772-502-4 US-11-73-502-4	US-09-819-104A-5 US-09-815-242-12713 US-09-738-877-3 US-09-961-403-13 US-10-153-668-212 US-10-757-781-62	US-09-785-548-13 US-09-785-548-43 US-09-291-417-13 US-09-862-179A-44 US-10-177-293-86 US-09-291-44-199	US-10-294-804-2 US-10-118-513A-2 US-10-118-513A-8 US-10-102-555-2 US-09-771-161A-224 US-09-771-161A-225
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ALIGNMENTS

ö 61 KERHKAQPTQMPPFSGITELVNNVLQPQOKQPNEKEPQTYLHQQPEMTKEQVXKNGEESQ 120 6.1 KEKHKAQPIQWEPPSGITELWNNVLQPQQKQPNEKEPQIYLHQQPEMYKEQVKNGEESQ 120 121 QQQBQKGDAPTCGICHKTKFADGCGHNCSYCQTKPCARCGGRVBLRSNKVMWVCNLCRKQ 180 9 9 1 MSAPLGPRGRPAPTPAASQPPPQPEMPDLSHLTEERRKTILAVMDRGRGEERRGSVLKT 1 MSAPLGPRGRPAPTPAASQPPPQPEMPDLSHLTEERRKIILAVMORQKKEEKEGSSVLKI Gaps Query Match
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1590; Conservative 0; Mismatches n. Thall. Sequence 1. Application US/10180326
Publication No. US20030049661A1
GENERAL INFORMATION:
APPLICANT: Seino, Susumu
APPLICANT: Shibasaki, Tadao
APPLICANT: OZAKi, No. US20030049661Aluaki
ITLE OF INVENTION: Protein Rim2
FILE REFERENCE: P21573
CURRENT APPLICATION NUMBER: US/10/180,326
CURRENT FILING DATE: 2002-06-27
FRIOR APPLICATION NUMBER: J 208372/99
FRIOR FILING DATE: 1999-10-08

PRIOR FILING DATE: 1999-10-08
5

NUMBER: OF SEQ ID NOS:
5

SEQ ID NO 1
5 TYPE: PRT ORGANISM: Mus musculus 1590 US-10-180-326-1 LENGTH: 윱 ò 셤 Š ò

Db 1161 GSERPRGNEXISVTSKWANGAVSGKNLIKSTSISGDWCSLEKNDGSGSDTAVGALGT 1320 Qy 1321 SGKKRESSIGARWALVGLSKRSRSAGLSGTRSGGRKCSLEKNDGSGSDTAVGALGT 1380 Db 1321 SGKKRESSIGARWALVGLSKRSRSASGLSGTRSGGRKCLRSTVGRSTRFGLAVERNINGT 1380 Qy 1381 RQASRESTDGSMNSYSSEGHLIPPGVRLASDSGPSDFLDGLGPAGLVGRGTLATPAWGD1 1440 Db 1381 RQASRESTDGSMNSYSSEGHLIPPGVRLASDSGPSDFLDGLGPAGLVGRGTLATPAWGD1 1440 Qy 1441 QVGAMDKKGGLEVEIIRARGLVVKPGSKTLAPAPYVKVYLLDNGVCLAKKKTKVARKTLEP 1500 Db 1441 QVGAMDKKGGLEVEIIRARGLVVKPGSKTLAPAPYVKYYLLDNGVCLAKKKTKVARKTLEP 1500 Qy 1501 LYQQLLSFERSPQGRVLQIIVWGDYGRMDHKSFMGVAQILLDELELSNAVIGHFKLFPPS 1560 Db 1561 LYQQLLSFERSPQGRVLQIIVWGDYGRMDHKSFMGVAQILLDELELSNAVIGHFKLFPPS 1560 Db 1561 SLYDPTSAPLTRRASGSSLESSTGPSYSRS 1590 Db 1561 SLYDPTSAPLTRRASGSSLESSTGPSYSRS 1590	RESULT 2 US-10-144-62 US-10-144-194A-62 Sequence 62, Application US/10144194A Publication No. US20030215809A1 GENERAL INFORMATION: TITLE OF INVENTION: Regulated Breast Cancer Genes TITLE OF INVENTION: Regulated Breast Cancer Genes FILE REFERENCE: 3U 103 R1 FILE REFERENCE: 3U 103 R1 CURRENT APPLICATION UNBER: US/10/144,194A NUMBER OF SEQ ID NOS: 114 SOFTWARE: Patentin version 3.0 BEQ ID NO 62 LENGTH: 3051 TTPE: PRT ORGANISM: Homo Sapien8 US-10-144-194A-62	Query Match 3.5%; Score 290.5; DB 12; Length 3051; Best Local Similarity 18.3%; Pred. No. 2.2e-08; Matches 349; Conservative 260; Mismatches 698; Indels 603; Gaps 79; QY 11 PAPTPAASQPPPQPEMPD	Db 131 IDRIISQVDPKINHTFRPQVEKAVHEFLATLANHKERGGGTTAPDTEKPDTSLITGGY 188 Qy 130 PTCGICHKTKPADGCGHNCSYCQTKPCARCGGRVSIASHNYMWCNLCRKQGEILTKSGA 189 Db 189 PTPGPSANV
181 QRILTKSGAMFYNSGSNTL,OQPDQKVPRGLRNERAPOEKKAKLHBQPOPOGAPCDLSVPA 240 181 QRILTRSGAMFYNSGSNTL,OQPDQKVPRGLRNERAPOEKKAKLHBQPOPOGAPCDLSVPA 240 241 VEKGRAHGLTRQDTTRNGSGVKHQIASDWPSDRKRSPSVSRDQNRRYEGSERREDYSGTV 300 241 VEKGRAHGLTRQDTTRNGSGVKHQIASDWPSDRKRSPSVSRDQNRRYEGSERREDYSGTV 300 301 PSDGTMPRSPSDYADRRSGREPQFYBEPGHLNYRDSNRRGHRHSKEYTVDDEDVESRDEY 360 302 PSDGTMPRSPSDYADRRSGREPQFYBEPGHLNYRDSNRRGHRHSKEYTVDDEDVESRDEY 360 303 PSDGTMPRSPSDYADRRSGREPQFYBEPGHLNYRDSNRRGHRHSKEYTVDDEDVESRDEY 360 304 PSDGTMPRSPSDYADRRSGREPQFYBEPGHLNYRDSNRRGHRHSKEYTVDDEDVESRDEY 360 305 PSDGTMPRSPSDYADRRSGREPQFYBEPGHLNYRDSNRRGHRHSSKYTUDDEDVESRDEY 360 306 ERQRREBEYQARYRSDPNLARYPVKPQPYEBGMR1HAEVSRARHERRHSDVSLANAELED 420 420 SKISLLRMDRPSRQRSVSERRAAMENQRSYSMERTREAQQSSSYPQRTSNHSPPTPRRSP 480 421 SRISLLRMDRPSRQRSVSERRAAMENQRSYSMERTREAQQSSSYPQRTSNHSPPTPRRSP 480 421 FIPLDRPDMRRADSLRRQHHLDPSSAVRKTKRENMETMLRNDSLSSDQSESVRPPPPRFRK 540 481 IPLDRPDMRRADSLRRQHHLDPSSAVRKTKRENMETMLRNDSLSSDQSESVRPPPRFRK 540	S41 SKKGGRANRQVSLSSSERELASTPETTSCDDVELESESVBRKGDSQKGRRKTSEQGVLSDS 600 541 SKKGGRANRQVSLSSSERELASTPETTSCDDVELESESVSEKGDSQKGRRKTSEQGVLSDS 600 601 NTRSERQKKRNYYGGHSLEEDLEWSEPQ1KDSGVDTCSSTTLWERSTSDKHPVTWQPSK 660 601 NTRSERQKRNYYGGHSLEEDLEWSEPQ1KDSGVDTCSSTTLWERSHSHSDKHPVTWQPSK 660 601 NTRSERQKRNYYGGHSLEEDLEWSEPQ1KDSGVDTCSSTTLWERSHSHSDKHPVTWQPSK 660 601 NTRSERQKRNYYGGHSLEEDLEWSEPQ1KDSGVDTCSSTTLWERSHSHSDKHPVTWQPSK 660 601 DGDRLIGRILLWKRLKDGSVPRDSGAMLGLKVVGGKTTESGRLCAFITKVKKGSLADTVG 720 601 DGDRLIGRILLWKRLKDGSVPRDSGAMLGLKVVGGKTTESGRLCAFITKVKKGSLADTVG 720 721 HLRPGDEVLEWNGRLLQGATFEEVYNIILESKDEPQVELVVSRPIGDIPRIPDSTHAQLE 780 721 HLRPGDEVLEWNGRLLQGATFEEVYNIILESKDEPQVELVVSRPIGDIPRIPDSTHAQLE 780 721 HLRPGDEVLEWNGRLLQGATFEEVYNIILESKDEPQVELVVSRPIGDIPRIPDSTHAQLE 780 721 HLRPGDEVLEWNGRLLQGATFEEVYNIILESKDEPQVELVVSRPIGDIPRIPDGTHAQLE 780 721 HLRPGDEVLEWNGRLLQGATFEEVYNIILESKDEPQVELVVSRPIGDIPRIPDGTHAQLE 780 721 HLRPGDEVLEWNGRLLQGATFEEVYNIILESKDEPQVELVVSRPIGDIPRIPDGTHAQLE 780 721 HLRPGDEVLEWNGRLLQGATFEEVYNIILESKDEPQVELVVSRPIGDIPRIPDGTHAQLE 780 721 HLRPGDEVLEWNGRLLQGATFEEVYNIILESKDEPQVELVVSRPIGDIPRIPAGLE 780 721 HLRPGDEVLEWNGRLUGGATFEEVYNIILESKDEPQVELVVSRPIGDIPRIPAGLE 780 721 HLRPGDEVLEWNGRLUGGATFEEVYNIILESTRAFFER 780 721 HLRPGDEVLEWNGRLUGGATFEEVYNIILESTRAFFER 780 721 HLRPGDEVLEWNGRLUGGATFEEVYNIILESTRAFFER 780 721 HLRPGDEVLEWNGRLUGGATFER 780 721 HLRPGDEVLEWNGRLUGGATFER 780 780 HLRPGDEVLEWNGRLUGGATF		1021 SPSGSPHRVDVIGRIRSWSPSAPPORNVEGGHRGTRATCHYNTISRWDRHRVWDDHYSS 1080 1021 SPSGSPHRVDVIGRIRSWSPSAPPORNVEGGHRGTRATCHYNTISRWDRHRVWDDHYSS 1080 1021 SPSGSPHRVDVIGRIRSWSPSAPPORNVEGGHRGTRATCHYNTISRWDRHRVWDDHYSS 1080 1081 DRDRDCRAADRQPYHRSRSTRORPLIERTTTRSRSSERPDTNIARSWPSLATGRSAPPSP 1140 1081 DRDRDCRAADRQPYHRSRSTRORPLIERTTTRSRSSERPDTNIARSWPSLATGRSAPPSP 1140 1141 ALSRSHPRTGSVQTSPSSTPGTGRRQDLPQLPPKGTLERSAMDIERRRQMKLAKYKOV 1200 1141 ALSRSHPRTGSVQTSPSSTPGTGRRQDLPQLPPKGTLERSAMDIERRRQMKLAKYKOV 1200 1141 ALSRSHPRTGSVQTSPSSTPGTGRRGQLPQLPPKGTLERSAMDIERRRQMKLAKYKOV 1200 1201 AGSDPRLRQDYHSKYRSGWDPHRGADTVSTKSSDSDVSDVSAVSRTSSASRFSSTSYMSV 1260 1201 AGSDPRLRQDYHSKYRSGWDPHRGADTVSTKSSDSDVSDVSAVSRTSSASRFSSTSYMSV 1260 1261 QSBRPRGNRKISVPTSKMONRQMGVSGKNLTKSTSISGDMCSLEKNDGSQSDTAVGALGT 1320

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Oy 1166 Db 1371 QATLL	Qy 1215 YRS Db 1430 VENGK	1256	1300	1342	Oy 1387 8TDGS Db 1662 KCDGG Qy 1426 LVGRQ Db 1722 BTBGT	RESULT 3 US-10-177-293-423 ; Sequence 423, Ap. ; Publication No. ; GENERAL INPORMAT	; APPLICANT: LILLI ; APPLICANT: Zhac ; APPLICANT: Zhac ; APPLICANT: Gann ; APPLICANT: Kame	in to the th	APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT:	APPLICANT: APPLICANT: TITLE OF INV TITLE OP INV PILE REFEREN CHRENT APPL	PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR	PRIOR ; PRIOR ; PRIOR ; PRIOR ; PRIOR		; NUMBER OF SEQ II ; SOFTWARE: PastSE ; SEQ ID NO 423 ; LENGTH: 3664
314ADRRSQREPQFYEEPGHLNYRDSUR338 314	339RGHRHSKEYIVDDEDVESRDEVERQRREERYQARYRSDPNIARYPVKPQP 388 1	YERQMRIHARVSRARHERRHSDVSLANAELEDSRISLLRMDRPSRQRSVSERRAAMEN : : :: ::	447 QRSYSMERTREAGGQSSYPQRTSNHSPPTP-RRS 479	480 PIPLDRPDWRRADS-LRKQHHLDPSSAVRKTKR	516 TMLRNDS-LSSDQSESVRPPPPRPHKSKKGGKGR 548	LSDSNTRSERQKKRMYYGGHSLEEDLEMSEPQIKDSGVDTCSSTTLABEHSBSDKHPVTM	865 QRRSESYSEDKCDMDSTNMDSNLKPERVUHKEKRRTKSLLERKLVLKSKSKT 916 709 KVKKGSLADTVGHLRPGDEVLEMNGRLLQGATFEEVYNIILESKDEPQVELVVSR 763 : : : : :	764PIGDIPRIPDSTHAQLESSSSFPESQKWDRPSISVTSPWSPGMLRDVPPLSGGQLS 819	820 IKLWFDKVGHQLIVTILGAKDLPSREDGRPRNPYVKIYFLPDRSDKNKRRTKTVKKTLEP 879		994SDYRHNGRDLQSSTLSVPEQVMSSNH 1019 - - - - - - - - -	1020 CSPSGSPHRVDVIGRTRSMSPSAPPPQRNVEQGHRGTRATG-HYNTISRMDRHR 1072 1192 NSEKHADHRSTLTKKMHIQSAVSKMNPGEKEPIHRGTTEVNIDSETVHRMLLSAPSENDR 1251	1073 VMDDHYSSDRDRDCRAADRQPYHRSRSTEQRPLLERTTTRSRSSERPDTWLMRSMPSLMT 1132 1252 VQKWLKWTAAERHVAQSDATLEHSTNLDSSPSLSSVTVVPLRESYDPDV1PLFDKRTVLE 1311	1133 GRSAPPSPALSRSHPRTGSVQTSPSSTPGTGRR 1165
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66GROLPQLPPKGTLERSANDIRERNROMKLNKYKQVAGSDPRLEQDYHSK 1214 	15 YRSGMDFHRGADTVSTKSSDSDVSBVSA-VSRTSSASRFSST 1255 : :	56 SYMSVQSER PRGNRKISVFTS-KMQNRQMGVBGKNLTKSTSISGD 1299 	00MCSLEKNDGSQSDTAVGALGTSGKKRRSSIGAK	42 KSRSASQLSQTBGGGKKLRSTVQRSTETGLAVEMRNWMTRQASRE 1386 03 SETFLTSTKKKRSGRCAVARSEDRAADL-TAVHAVKIRANVHSVVTEKKDDAVTSAGSRE 1661	STDGSRNSYSSECRLIFPCVKLASDSQFSDFLDGLGPAQ	1662 KCDGSLGRDSEIVEGTITFISEVESDGAVTSAGTEIRAGSISSEEVDGSGCANMARAGPKK 1721 1426 LVGROTLATPAMGDIOWGAMMPKKGOLKVEITRARGIVVKPGS 1467	22 BTBGTVTCTGARGREDNFVICSVTGAGPREERMVTGAGVVLGDNDAPPGT 1771	RESULT 3 Sequence 423 Application 19/10171293 Sequence 423 Application No. US20030124128a1 GENERAL INCRRAITION: GENERAL INCRRAITION: GENERAL INCRRAITION: APPLICANT: Glant, Karen APPLICANT: Glant Annuaratu, Manjula APPLICANT: Glant Annuaratu, Manjula APPLICANT: Glant Annuaratu, Manjula APPLICANT: Manthar, Shubhangi APPLICANT: Manthar, Shubhangi APPLICANT: Mang, Youzhen APPLICANT: Myez, N. Conyoo APPLICANT: Myez, N. Conyoo APPLICANT: Myez, N. Conyoo APPLICANT: Myez, N. Conyoo APPLICANT: Myez, N. Conyoo APPLICANT: Myez, N. Conyoo APPLICANT: Myez, N. Conyoo APPLICANT: Myez, N. Conyoo APPLICANT: Meyers, N. Conyoo APPLICANT: Meyers, N. Conyoo APPLICANT: Meyers, N. Conyoo APPLICANT: Mills, Goodon B TITLE OF INVENTION: COMPOSITIONS, KITS, AND METHODS FOR IDENTIFICATION, APPLICANT: Mills, Goodon B TITLE OF INVENTION NUMBER: US 60/306,501 PRIOR APPLICATION NUMBER: US 60/306,501
1166	1215	1256	1300	1342	1387	1662	1722	RESULT 3 18-10-177-293-423 18-10-177-293
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A 6	S 8 6	ජි සි · 	<i>장</i> 음 ·	ਲੇ · ਜ਼ਿੰ 	장 ·윰 ───	& 8	장 옵	රි සි	<i>장</i> 옵	& A &	· 음·	ර් සි රි	8 8 8 8	X D	** ** ** ** **
; TYPE: PRT ; ORGANISM: Homo sapiens US-10-177-293-423	Query Match 3.4%; Score 279; DB 15; Length 3664; Best Local Similarity 20.1%; Pred. No. 1.4e-07; Matches 370; Conservative 223; Mismatches 676; Indels 570; Gaps 85;	31 HLTEERKIILAVMDRQKKEERKEGSVLKIKBEHKAQPIQWFPPSGITELVNNVLQPQ 88	89 OKOPNEKEPOTKILHOOP-EMYKEOVKKWGEBSOOOGEKGD 128 :::	129 APTCGICHKTKFADGCGHNCSYCQTKFCARCGGRVSLRSNKVMWVCNLCRKQQBILTK 186 :	187 SGAMPYNSGSNTLOGPDOKVPRGLRNERAPQEKKARLHROPOPOGA 232 : : : : : 517 NCVMLDGLGSNVSDOXLTRHPCRYQPVVKVVPDRLKGMALVLYNEIRYAQA 567	PGDLSVPAVE - KGRAHGLTRQDTIKNGSGVK-HQIASDMESDR 	274 KRSPSVSRDQNRRYEQSEEREDYSQYVPSDGTMPRSPSDYADRRS 318 :		LARYPVKPQPYBEÇMRIHAEVSRAR-HERRHSDVSLANABLEDGRISILEWDRPSRQRSV	SERRAAMENORSYSMERTREAGGGSSYPQRTSNHSPPTPRRSPIPLDRPDMRRADSLRKQ	498 HHLDPSSAVRKTKREKMETMLRNDSLSSDQSESVRPPPPRPHKSKKGGRORGVSLSSS 555	EBELASTPRY-TSCDDVELESESVSEKGDSQKG 	SERQKKRMYYGGHSLEEDLEWSEPQIKDSGVDTCSSTTLAREHSHSDKHPYTWQPSKDGD :	932HLK 965 724 PGD	805 GMLRDVPQFLSGQLSIXLMFDXVGHQLIVTILGAKDLPSREDGRPRNPYVK-IYFL 859 1081 SSDLQARLG-ELAGESVENQEVQSKKPIPSKPQLKQLQVLDDQG 1123 860 PDRSDKNKRRIKTVKKTLEPKWNQTFIXSPVHRREFRERMLEITLWDQAR 909
; TYP! ; ORG! US-10-1;	Query Best Match	දු දු	දු පු	දු පු	<i>≿</i> 8	දු දු	<i>≿</i> 8	ඊ සි	8 8 8	1 & B	& A	g 25	9 64 64 64	a & a & a	\$ A & ,

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Sequence 34248, Application US/09864761

| Sequence 34248, Application US/09864761
| Patent No. UB2002004633A1
| GENERAL INFORMATION:
| APPLICANT: Penn, Sharron G. APPLICANT: Penn, Sharron G. APPLICANT: Penn, Sharron G. APPLICANT: Penn, Sharron G. APPLICANT: Penn, Sharron G. APPLICANT: Penn, Sharron G. TITLE OF INVENTION: WENEXE EXPRESSION ANALYSIS BY MICROARRAY
| TITLE OF INVENTION: HUMAN GENCE EXPRESSION ANALYSIS BY MICROARRAY
| TITLE OF INVENTION: HUMAN GENCE EXPRESSION ANALYSIS BY MICROARRAY
| TITLE OF INVENTION: HUMER: US/09/864,761
| CURRENT APPLICANTON NUMBER: US 60/180,312
| PRIOR FILING DATE: 2000-05-27
| PRIOR FILING DATE: 2000-05-26
| PRIOR FILING DATE: 2000-06-03
| PRIOR PLILING DATE: 2000-09-27
| PRIOR FILING DATE: 2000-09-27
| PRIOR FILING DATE: 2000-09-27
| PRIOR FILING DATE: 2001-01-30
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284 -----SETLRYNHNFEPKSKIVSPGLTIHERISE--KEHSLEDNSSPNSLEP----
                                                                       540 KSKKAGKMRQVSLSSSBKBLASTP-----EYTSCDDVELBSBSVSEKGDSQKGKKK
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FILING DATE: 2001-01-30
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APPLICANT: Sahin, Aysegul
APPLICANT: Mills, Gordon B.
ITILE OF INVENTION: COMPOSITIONS, KITS, AND METHODS FOR IDENTIFICATION, ASSESSMENT,
ITILE OF INVENTION: PREVENTION, AND THERAPY OF BREAST CANCER
FILE REPERENCE: MI-038
CURRENT FILING DATE: 2002-06-21
PRIOR APPLICATION NUMBER: US 60/299,887
PRIOR PILING DATE: 2001-06-21
PRIOR PILING DATE: 2001-06-21
PRIOR PILING DATE: 2001-06-27
PRIOR PILING DATE: 2001-06-27
PRIOR APPLICATION NUMBER: US 60/306,501
PRIOR PILING DATE: 2001-07-18
PRIOR PILING DATE: 2001-09-25
PRIOR APPLICATION NUMBER: US 60/325,002
PRIOR PILING DATE: 2002-03-05
PRIOR PILING DATE: 2002-03-05
PRIOR PILING DATE: 2002-03-05
PRIOR PILING DATE: 2002-03-05
PRIOR PILING DATE: 2002-03-05
PRIOR PILING DATE: 2002-05-14
NUMBER OF SEQ ID NOS: 506
SOFTWARE: FRAESEQ for Mindows Version 4.0
SEQ ID NO 449
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al Similarity 18.7%; Pred. No. 2.3e-08;
195; Conservative 157; Mismatches 302; Indels 389;
                                                                                                                                               Bast Jr., Robert C.
Hortobagyi, Gabriel N.
Pusztai, Lajos
Meric, Funda
                                     ersch, Sebastian
nahan, John
                                                                                                             Meyers, Rachel B.
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US-10-177-293-449
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                                                                                                                                                     353 ADGVSAVDLEKLEARKRRFADSNLKAEKOKPEVKKSSPEMEDARVLSKKOPDVSSREVIL 412
                                                                                                                                                                                                                                                                                               SRPIGDIPRIPDSTHAQLESSSSFESQIMDR ***** PSISVTSPMSPGMLR 808
                                                                                                                                                                                                                                                                                                                                                                                                413 IRE-GEAERKP----VRKEILKRESKKIKLDRINTVASPKDCQELASISVGSGSRPS--- 464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             --SDLQARLG-ELAGESVENQ---EVQSKKPIPSK-----PQLKQLQVLDDQGPERE 510
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                                                                    --EVYNIILESKPEPQV---ELVV 761
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DVPQFLSGQLSIKLWFDKVGHQLIVT1LGAKDLPSRRDGRPRNPYVK-IYFL----PDRS
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OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 10

OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 8.9

OTHER INFORMATION: EXPRESSED IN FOLKENIA, SIGNAL = 4.8

OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 14

OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 7.2

OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 9.5

OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 9.3

OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 9.3

OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 7.1

OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 7.7

OTHER INFORMATION: EXPRESSED IN HELAO, SIGNAL = 7.7

OTHER INFORMATION: EXPRESSED IN HALAO, SIGNAL = 7.7

OTHER INFORMATION: EXPRESSED IN BIATO, SIGNAL = 7.7

OTHER INFORMATION: EXT HUMAN HIT: POR640, EVALUE 3.00e-10
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3.3%; Score 270.5; DB 9; Length 2665;
Best Local Similarity 20.6%; Pred. No. 3e-07;
Matches 316; Conservative 182; Mismatches 584; Indels 453;
PRIOR APPLICATION NUMBER: PCT/USO1/00668
PRIOR FILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR PLING DATE: 2001-01-30
PRIOR PLING DATE: 2001-01-30
PRIOR PLING DATE: 2001-01-30
PRIOR PLING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/USO1/00661
PRIOR APPLICATION NUMBER: PCT/USO1/00670
PRIOR PILING DATE: 2001-01-30
PRIOR PLING DATE: 2001-01-30
PRIOR PLING DATE: 2000-09-21
PRIOR PLING DATE: 2000-09-21
PRIOR PLING DATE: 2000-09-21
PRIOR PLING DATE: 2000-09-29
PRIOR PLING DATE: 2000-06-30
PRIOR PLING DATE: 2000-06-30
PRIOR PLING DATE: 2000-06-30
PRIOR PLING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SEQ ID NOS: 49117
SEQ ID NO 34248
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ORGANISM: Homo sapiens
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                                              559 HIQFALEYVESLKELHVFVAQCKOLAAADVKKQRSDPYVKAYLLPDKGKQKKKTLVVKK 618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            203 RSKLSPSPSLRKSSKSKRKKSSPKSSSASKKDRKTSAVSSPLLDQQRN8-----KTN 254
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          179 KOQEILTKSGAWFYNSGSNTLOQPDQKVPRGLRNEEAPQEKKAKLHEQPQFQGAPGDLSV 238
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-------QLIVIIIGAKDLPSREDGRPR-NPYVKIYFLPDRSDKNKRRTKIVKK 875
                                                                                                                                                       876 TLAPKWNOTPIYSPVHRREFRERMLEITLWDOARVREEBSBFLGEILIELETALLDDBPH 935
                                                                                                                                                                                                          62 REHKAQPTQWPPPSGITELVANVLQPQQKQPWEKEPQTKLHQQPEMYKEQVKKMGEESQQ 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      352 KR----TPSPSY-----QRTLTPP-----LRRSASPYPSHSL--SSPQRKQSPPRHRS 393
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  298 QYVPSDGTMPRSPSDYADRRSQREPOFYEEPGHLNYRDSNRRGHRHSKRYIVDDEDVESR 357
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8 RGRPAPTPA---ASQPPPQPEMPDLSHLTEEERK.--IILAVMDRQKKEEEKEGSVLKIK 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 3.1%; Score 258.5; DB 12; Length 1564; Best Local Similarity 18.9%; Pred. No. 7.8e-07; Matches 286; Conservative 214; Mismatches 552; Indels 459; Gaps
                                                                                                                                                                                                                                                                                                                            936 ----WYKLOTHD-------VSSLPLPRPSPYLP 957
                                                                                                                                                                                                                                                                                                                                                                                                        676 KOLRWYPLKRKTAPVALEAENRGEMICLALQYVPEPVPGICILP 717
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2, Application US/10144198

Publication No. US20030219748A1

GENERAL INFORMATION:

TITLE OF INVENTION: Regulated Prostate Cance Genes

FILE REPERENCE: 90 105 R1

CURRENT PELLICATION NUMBER: US/10/144,198

CURRENT FILING DATE: 2002-05-14

SUPPRESE PATENTIN VEST 44

SOPPHARE: Patentin version 3.0
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 1564
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830
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8
                                                                                                Sequence 492, Application US/10339782

Publication No. US20030166026A1

GENERAL INPORMATION:

APPLICANT: Lyux Therapeutics, Inc.

APPLICANT: Bowen, Benjamin A

TITLE OF INVENTION: Identification of Specific Biomarkers for Breast Cancer Cells;

TITLE OF INVENTION: Undentification of Specific Biomarkers for Breast Cancer Cells;

TITLE OF INVENTION: Undentification of Specific Biomarkers for Breast Cancer Cells;

CURRENT APPLICANTON NUMBER: US/10/339,782

CURRENT FILING DATE: 2003-01-08

NUMBER OF SEQ ID NOS: 495

SEQ ID NO 492

LENGTH: 862
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  247 HGLTRODTIKNGSGVKH-QIASDMPSDRKRSPSVSRDQNRRYBQ-----SERRED 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              76 AAPASPSSSVVNPASSVIDMSQENTKKPNSPEK-RKNPPNSSKLPEGHSSQOTKNEQSK 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             464 YPQRTSNHSPPTPRRSPIPLDRPDMRRADSLRKQHHLDPSSAVRK---TKREKMSTMLRN 520
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |:: :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | :: | | :: | :: | | :: | :: | | :: | :: | | :: | :: | | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | ::
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   741 FEEVYNIILESKPEPQVELVVSRPIGDIPRIPDSTHAQLESS-----SSSFESGKWDR-- 793
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 - EEEPSPVLXTLERSAARKMPSKSLEDISS-DSSNQAKVDNQPEELVRSAEDDEKPDQXP 498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----PSISV--TSPMSP-----GMLRDVPQFLSGQLS---IKLWFDKVGH----- 829
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          277;
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US-10-339-782-492
                                     RESULT 6
US-10-339-782-492
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                                                                                     765 BRERERERERERERARERDKERERORDWED---KOKGRD---DRREKREEIREDRNP---- 813
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                        603
                                                                                                                                                                                       VVRPQE-SRSLSPSHLTED------RQGRWKBE-----DRKPE----- 897
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                                       S----EROKKRMYYGGHSLEEDLEWSEPOIKDSGVDTCSSTTLNEEHSHSDKHPVTWQP
                                                                                                                   SKDG--DRLIGRILLIN-----KRLKDGSVPRDSGAMLGLKVVGGKMTESGRLCAF
                        571 VELESESVSEK-------GDSQKGKRKTSEQGVLSDSNTR
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Sequence 4, Application US/10144198
Publication No. US20030219748A1
GENERAL INFORMATION:
APPLICANT: OriGene Technologies Inc

RESULT 8 US-10-144-198-4

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TITLE OF INVENTION: Regulated Prostate Cance Genes FILE REFRENCE: 90 105 R1
CURRENT APPLICATION NUMBER: US/10/144,198
CURRENT FILING DATE: 2002-05-14
NUMBER OF SEQ ID NOS: 44
SOFTWARE: Patentin version 3.0
SEQ ID NO 4
                                                                                                                                                                                     LENGTH: 1564
TYPE: PRT
CRGANISM: Homo sapiens
US-10-144-198-4
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	CY 826 KVGHQLIVTILGAKDLPSREDGRPRNPYVKIYFLPDRS-DKNKRRIKTVKKTLEPKNNOT 884	- <u>¥</u>	885 F: :: :: :: :: : :: : : :: : :: : : :: : : :: : : : : : : : : : : : : : : : : : :	Db 975 VGIERGNIETTSEDGQVFSPKKGQKKKSIEKKRKKKKKGKGDSDI 1016	930 LDDEPHWYKLQTHDVSSLPLPRPSPYLPRRQLHGESPTRKLQRSKR1SDSGVSDYD		986 CEDGVGVVBDYRHNGRDLQSSTLSVPEQVMSSNHCSPSGSPHRVDVIGRTR8-WSPSA	DD 1069 DEDVPDRIEVIEAEHTATATTPGSTPSFLSSLL 1101	Cy 1043 PPPQR	TIOS EEEEEVATAINITIENTINATUREDIODITIOTORIETUTA.	CHRTRVEKVETDINSSLEDVEN STATES	1125 RSMPSIMTGRSAPPSPALSRSHPRTGSVOTSPSSTPGTGRRGROLPQLP	: 1207 RSPSNDSAHRSGDDQSGRKRVLHS	QY 1174 PKGTLERSAMDIEERNRQMCLNKKKQVAGSDFRLEGDY 1211	DD 1260 SRSTSSDRQDSRSHSSRRSSPRGVHSRSGSPDSRDKLQRRDKYEHDREKERER 1315	CY 1212 HSKYRGGNDPHRGADTVSTKSSDSDVSDVSAVSRTSSASRFSSTSYMGVQSERPRGN 1268	DD 1316 RDTROREWDRDADKDWPRNRDRDRLRERERERERDKRKDLDRERERLISDSVERDRDR 1373	LTKSTSISGDMCSL	Db 1374 DRDRTFESSQIESVKRCKAKLEGEHERDLESTSRDSLALDKERWDKDLGSVQGFEDT 1430	Qy 1321 SGKKRRSSIGA 1331	Db 1431 NKSERTESLEA 1441	e titisad	US-09-987-482-1 ; Sequence 1, Application US/09987482	; Publication No. US20020184656A1 ; GENERAL INFORMATION:	; APPLICANT: BHANDAR, POONAM	; TITLE OF INVESTIGATION: IN VIVO ASSAY SYSTEM POR SCREENING AND VALIDATION OF	; FILE OF INVENTION: DRUGS AND OTHER SUBSTANCES ; FILE PREPREDENT: 056859-0134 ; FILE PROPERTY 1000000000000000000000000000000000000	CURRENT FILING DATE: 2002-03-21	Patentin Ve	; SEQ ID NO 1	; TYPE: PKT ; Homo sapiens TS-09-987-482-1	Diery Match 3 18.	Indela	

30 SHLTEBERKIILAVMDRQKKEREKRQSVLKIKEEHKAQPTQWFPFSGITELVNNVLQPQQ 89

:| ||: 1563 LLDDSDDDIELLEBCIISAMPTKSSKKAKKPAQTASKLPPVAKKPSQL-----PVYK 1616 1715 DNKARBGDILABCINSAMPKGKSHKPFRVKKIMDQVQ-QASASSSAPNKNGLDGKKKKRP 1773 1806 SDNYDSKXQNLKNNSKDPNDKLPNNEDRVRGSPAPDSPHHYTPIEGTPYCPSRNDSLSSL 1865 1012 NHWDDANDGELDTPINYSLKYSDRQ----LNSGRQSPSQWERWARPKHIIR--DEIKQSRQ 1065 1357 GAKSPEKSGAQTPKSPPRHYVQSTPLMPSRCTSV8----BLDSFRSKSIASSVQSEPCSG 1412 1452 ---VPROKAPTABKRES-----GFKQAAVNAAVQKVQVLPDADTLLHFATESTPDGFSC 1502 1503 SSSLSALSLDEPPIQKDVELAIMPPVQENDMGNETESEQPKEGNENQEKEAEKTIDSEKD 1562 1617 LLPSQNRLQPQKH-VSFTPGDDMPRVXCVBGTPINFSTATSLSDLTIBSPPNKLAAGBGV 1675 1113 N------RVGSNHGINQNVSQSLC----QEDDYEDDKPTNYSERYSEREGHER-- 1155 514 METMIRNDSIASDOSESVRPPPPRPHKSKKGGKMRQVSIASSEEEL----ASTPEYTSC 568 691 KVVGGRMTESGRLCAFITKVKKGSLADTVGHLRPGDEVLEMNGRLLQGATFEEVYNIILE 750 751 SKPEPQVELVV----SRPIGD-----IPRIPDSTHAQLESSSSFESGKWDRPSISVT 799 800 SPMSPGMIRDVPQFLSGQLSIKLWFDKVGHQLIVTILGAKDLPSREDGRPRNPYVKIYFL 859 PSPYLPRRQL------HGESPTRRLQR------SKRISDSEVSDYDCE---- 987 SRDEYERGRREEEYQARYRSDPNLARYPVKPQPYEEGMRIHAEVSRARHERRHSDVSLAN 415 416 AELEDGRISLLRMDRP----- SRQRSVSERRAAMENQRSYSMERTREAQ---- 459 ----GOSSYPORTSNHSPPTPRRSPIPLDRPDMRRADSLRKQHHLDPSSAVRKTKRKK 513 596 VLSDSN------TRSERQKKRMYYGGHSLEEDLEMSEPQIKDSGVDTCSS 639 640 TTLANERHSHSDKHPVTWQPSKDGDRL--IGRILLN-----KRLKDGSVPRDSGAMLGL 690 860 PDRSDKNKRRTKTVKKTLBPK------RR 893 KOPNEKEPOTKIHOOPEMYKEQVKKMGEESQQ---QQSQKGDAPTCGICHKTKFADGCGH 146 147 NCSYCOTKFCARCGGRVSLRSNKVMWYCNLCRKQQRILINSGAMFYNSGSWTLQQPDQKV 206 267 SOMPSDRKRSPSVSRDQNRRYBQSBEREDYSQYVPSDGTMFRSPSDYADRRSQREPQFYB 326 327 BPGHLMYRDSNRRGHRHSKR----YIVDD-------BDVB 355 207 PRGLRNERAPOEKKAKLHEQPQFQGAPGDLSVPAVEKGRAHGLIRQDTIICNGSGVKHQIA 266 8 셤

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                                   ---RDLQSSTLSVPRQVMSSNHC 1020
                                                                                                            SPSGSPHRVD----VIGRIRSWSPSAPPPQRNVEQGHRGIRATGHYNTISRMD-RHRVMDD 1076
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1923 PKPILQKQSTPPQSSKOIPDRGAATDEKLQNFAIENTPVCFSHNSSLSSLSDIDQENNNK 1982
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APPLICANT: Takaaki Sato and Junn Yanagisawa
TITLE OF INVENTION: COMPOUNDS THAT INHIBIT THE INTERACTION BETWEEN
TITLE OF INVENTION: COMPOUNDS THAT INHIBIT THE GLGF
TITLE OF INVENTION: SIGNAL-TRANSDUCING PROTEINS AND THE GLGF
TITLE OF INVENTION: (PDZ/DHR) DOMAIN AND USES THEREOF
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSER: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
CITY: New York
COUNTRY: New York
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ATTORNEY AGENT INFORMATION:
NAME: White, John P
RESISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 0575/48962/JPW/JKM
                                     ---DGVGVVSDYRHNG-
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Publication No. US20020058607A1
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2484 LSPSLPDMSLSTHSS 2498
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                                                                                                                                                                                                                                                    Query Match 3.1%; Score 257.5; DB 8; Length 2843; Best Local Similarity 18.0%; Pred. No. 2e-06; Matches 305; Conservative 238; Mismatches 617; Indels 535;
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
TELEPAX: (212) 391-0525
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
LENGTH: 2843 amino acids
                                                                                                                           TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
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                                                                                                                                                           1774 SPVKP----IPQNTEYRTRV--------RKNADSKNILMAERVF 1805
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                                                                                           SPMSPGWLRDVPQFLSGQLSIKLWFDKVGHQLIVTILGAKDLPSREDGRPRNPYVKIYFL 859
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RESULT 11
US-10-092-138-30

Sequence 30, Application US/10092138

Publication No. US20030170723A1

GENERAL INFORMATION:

APPLICANT SATO, TAKA-Aki

ITILE OF INVENTION: METHOD OF PREPARING A PROTEIN ARRAY BASED ON

TITLE OF INVENTION: BIOCHEMICAL PROTEIN INTERACTION

FILE REPERRENCE: 65823/JPW/PT

CURRENT APPLICATION NUMBER: US/10/092,138

CURRENT FILING DATE: 2002-09-06

NUMBER OF SEQ ID NOS: 33

SOFTWARE: Patentin Ver. 2.1
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; SEQ ID NO 30 ; LENGTH: 2843 ; TYPE: PRT ; ORGANISM: hu US-10-092-138-30	1943 1843 1 Duman 1-30
Query Match Best Local 9 Matches 309	ch 3.1%; Score 257.5; DB 12; Length 2843; 11 Similarity 18.0%; Pred. No. 2e-06; 305; Conservative 238; Mismatches 617; Indels 535; Gaps 70;
φ _γ 30	SEERKIILAVMDRQKKEERKEQSVLKIKEEHKAQPTQWPPFSGITE
10	NEWDDINDGRLDTPINYSLKYSDBQLINSGRQS
Oy 90	OKOPHEKEPOTKLHQOFEMYTEGVKKWGEESQQQXBQKGDAPTGGICHKTKFADGCGH 146
Qy 147	NCSYCQTIRPCARCGGRUSLASHKVMWVCNLCRKQQBILLTKSGAMFYNSGSWTLQQPDQKV
Db 1113	
207	PRGIANERAPOEKKAKI.HEQPOPGGAPGDI.SVPAVEKGRAHGI.TRODTI.KNGSGVKHQI.A
•	SDMPSDRKRSPSVSRDQNRXYEQSKERRDYSOYVPSDGTMPRSPSDYADRRSOREPOP
Db 1185	TOIPSSQKQSFFFKSSSGKTRHWSSSSKNTSTPSSNAKRQMQLHPSSAQ 12
Qy 327	
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Qy 356	SRDEYERQRRZEEYQARYRSDPNLARYFVKPOPYEEÇARIHAEVSRARHEDVSLA
Db 1298	3 SANTLQIABIKKKIGTRSARDPVSEVPAVSQHPRTKSSKLQGS-SLSSBSARHKAVEFSS 1356
97 416	AKLEDSRISLIRMDRPSRQRSVSERR
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                                      1806 SDNKDSKKQNLKNNSKDFNDKLPNNEDRVRGSFAFDSPHYTFIEGTPYCFSRNDSLSSL 1865
                                                                                SPSGSPHRVD----VIGRTRSWSPSAPPPQRNVEQCHRGTRATGHYNTISRMD-RHRVMDD 1076
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                                                                                                                                                                                          2043 ISSAMPKKKKPSRLKGDNEKHSP-----RNM-GGILGEDLTLDLKOIQRPDSEHGISPD
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                                                                                                                                                                          -----BGVGVVSDYRHNG------RDLQSSTLSVPBQVMSSNHC
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Publication No. US20030203414A1

GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Sato, Taka-Aki

APPLICANT: Yangisawa. Junn

TITLE OF INVENTION: SIGNAL-TRANSDUCING PROTEINS AND THE GLGP (PDZ, TITLE OF INVENTION: SIGNAL-TRANSDUCING PROTEINS AND THE GLGP (PDZ, TITLE OF INVENTION: DOMAIN AND USES THEREOF

FILE REFERENCE: 48962-A-PCT-US

CURRENT FILING DATE: 1999-05-17

CURRENT FILING DATE: 1999-05-17

NUMBER OF SEQ ID NOS: 30

SOFTWARE: PATENTING DATE: 2.1

SEQ ID NO 30

LENGTH: 2843

TYPE: PRT

ORGANISM: human
              ---WNQTFIYSPVH---
              PDRSDKNKRRTKTVKKTLEPK-----
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                                                                      Gaps
Query Match 3.1%; Score 257.5; DB 12; Length 2843; Best Local Similarity 18.0%; Pred. No. 2e-06; Matches 305; Conservative 238; Mismatches 617; Indels 535;
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MARCUS, Gregory A. ZINGLER, Kurt A.

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Best Local Similarity 18.8%; Freq. No. 6.1e-0/;
Matches 184; Conservative 117; Mismatches 278; Indels 402; Gaps
               APPLICANT: LU, Yan Monique G.
APPLICANT: You Monique G.
APPLICANT: You Monique G.
APPLICANT: MARRAN Rajagopal
APPLICANT: MARRAN Bridget A.
APPLICANT: THANGAVELU, Kavitha
APPLICANT: THANGAVELU, Kavitha
APPLICANT: THANGAVELU, Kavitha
APPLICANT: THANGAVELU, Kavitha
APPLICANT: THANGAVELU, Kavitha
APPLICANT: THE REFERENCE: PF-0801 PCT
CURRENT APPLICATION NUMBER: US/10/311,626
CURRENT FILING DATE: 2002-12-17
PRIOR PILING DATE: 2002-12-17
PRIOR PILING DATE: 2002-12-17
PRIOR PILING DATE: 2000-10-10; 2000-11-28
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PERL PROGRAM
                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No. US20030186379A1 4728247CD1
                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                                                                                   SEQ ID NO 5
LENGTH: 671
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                     PKPILQKQSTFPQSSKDIPDRGAATDEKLQNFAIENTPVCFSHNSSLSSLSDIDGENNNK 1982
                                                                                                                                                -------DGVGVVSDYRHNG------RDLQSSTLSVPEQVMSSNHC 1020
                                                                                                                                                                     SPSGSPHRVD---VIGRTRSWSPSAPPPQRNVEQGHRGTRATGHYNTISRMD-RHRVMDD 1076
                                                                                                                                                                                                                                                        2043 ISSAMPKKKKPSRLKGDNEKHSP-----RNM-GGILGEDLTLDLKDIQRPDSEHGLSPD 2095
                                                                                                                                                                                                                                                                                             1077 HYSSDRDRDCEAAD------RQ-----RQ--------PYHRSRSTE 1101
                                                                                                                                                                                                                                                                                                                                   2096 SENFDWKAIQEGANSIVSSLHQAAAAACLSRQASSDSDSILSLKSGISLGSPFHLTPDOG 2155
                                                                                                                                                                                                                                                                                                                                                                        :: | :: | :: | :: | 2156 EKPPTSHKGERSTLETKKIESESKGIKGGKKVYKSLITGKVRSHSEISGQMKQ 2215
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1175 KGTLERSAMDIBERNROMICLNKYKOVAGSDPRLEQDYHSKYRSG---WDPHRGAD---- 1226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1227 TVSTKSSDSDVSDVSAVSRTSSASRFSSTSYMSVQSERPRGNRKISVFTSKMONROMSVS 1286
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                                                                       PSPYLPRRQL-----HGESPTRRLQR-----SKRISDSEVSDYDCE---- 987
BFRERMLRITLWDQARVREERSEFLGBILIELBTALLDDEPHWYKLQTHDVSSLPLPR-- 951
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85 LOPQOKOPNEKEPOTKLHQQFEMYKEQVKOMGER--SQQQQBQKGDAPTCGICH----- 136

3 BLIDLSFLSREKOLILSVLQR-----DEFVRKADEKR------IRRLKNYEL 43

25 EMPDLSHLTERERKIILAVMDRQKKEEEKRQSVLKIKEEHKAQPTQWPPFSGITELVNNV 84

3.0%; Score 252; DB 12; Length 671; 18.8%; Pred. No. 6.1e-07;

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74 SPKINICRGCNH-----LVCRDC----RIQESNGIWRCKYCAKEIELKKATGDWFY-- 120
                                                                                                                                                                                                                                                                                                 301 PSDGTMPR-----SPSDYADRRSQREPQ--FYEEPGHLMYRDSNRRGHR 342
                                                                                                                                     195 GSNTLQQPDQKVPRGLRNEEAPQEKKAKTHEQPQPQGAPGDLSVPAVEKGRAHGLTRQDT 254
                                                                                                                                                                  255 IKNGSGVKHQI-----ASDMPSDRKRSPSV-----SRDQNRRYEQSKKRKDYSQYV 300
                                                                                                                                                                                                                                                208 DSDSTSRRDSLDKSGLFPEWKKMSAPKSQVEKETQPGGQRVVVFVDEGEMIFKKKNTRKILR 267
                                                                                                                                                                                                                                                                                                                                                                                                                         268 PS-RYTKSVIDLRPRDVVHESGSLGD---RSKSVPGL-------300
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                                                      137 --KIKFADGCGHNCSYCQTKFCARCGGRVSLRSNKVMWCNLCRKQQBILTKSGAMFYNS 194
                                                                                                                                                                                                                                                                                                                                                                                 343 HSKEYIVDDEDVESRDEYERQRREEEYQARYRSDPNLARYPVKPQPYEEQMRIHAEVSRA 402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  403 RHERRHSDVSLANAELEDSRISLLRMDRPSRORSVSERRAAMENORS----YS----- 451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    452 MERTREACGOSSYPORTSN---HSPPTPRRSPIPLDRPDWRRADSLRKCHHLDPSSAVRK 508
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44 L-----TCARCQESLGRL 73
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Sequence 5, Application US/10311626
Publication No. US20030186379A1
GENERAL INFORMATION:
APPLICANT: INCLY GENOMICS, INC.
APPLICANT: TANG, Y. Tom
APPLICANT: TANG, Y. Tom
APPLICANT: CHAMIA, Narinder X.
APPLICANT: BAUGHN, Mariah R.

RAMKUMAR Jayalaxmi TRIBOULBY, Catherine M. LU, Dyung Aina M.

DAS Debopriya

APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:

BANDMAN, Ölga ELLIOT, Vicki S. NGUYEN, Danniel B BURRILL John D.

GANDHI, Ameena R. LEE, Ernestine A. XU, Yuming

APPLICANT: APPLICANT: APPLICANT:

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1519 IIVWGDYGRMDHKSFMGVAQILLDELELSNMVIGWFKLFPPSSLVDFTSAPLTRRASQSS 1578
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       249 EAH-----SDIKVYHE 277
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TITLE OF INVENTION: Differentially Regulated Prostate Cancer Genes
FILE REFERENCE: 9U 204 205 11.
CURRENT APPLICATION NUMBER: US/10/341,434
CURRENT FILING DATE: 2003-07-18
PRIOR PILING DATE: 2002-01-15
PRIOR PILING DATE: 2002-01-15
PRIOR FILING DATE: 2002-01-15
NUMBER OF SEQ ID NOS: 238
SOFTWARE: Patentin version 3.1
SEQ ID NO 236
LENGTH: 2440
                                                                                                                                                                                                                                                                                                                                             N: EXPRESEED IN LUNG, SIGNAL = 0.93
N: EXPRESEED IN LUNG MARROW, SIGNAL = 1.9
N: EXPRESEED IN BRAIN, SIGNAL = 1.9
N: EXPRESEED IN HEALIOO, SIGNAL = 1.6
N: EXPRESEED IN PLACEMYA, SIGNAL = 1.2
N: EXPRESEED IN HEARY, SIGNAL = 1.1
N: EXPRESEED IN HEARY, SIGNAL = 1.5
N: EXPRESEED IN HEARY, SIGNAL = 1.5
N: EXPRESEED IN HEARY, SIGNAL = 1.5
N: EXPRESEED IN HEARY, SIGNAL = 1.5
N: EXPRESEED IN HEARY, SIGNAL = 1.5
N: EXPRESEED IN BT474, SIGNAL = 1.5
N: EXPRESEED IN BT474, SIGNAL = 1.5
N: EXPRESEED IN BT474, SIGNAL = 1.5
N: EXPRESEED IN BT475, EVALUE 5.00e-22
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PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION UNDERR: US 09/774,203
PRIOR FILING DATE: 2001-01-29
NUMBER OF EEQ ID NOS: 49117
SOFTWARE: Annomax Sequence Listing Engine vers: 1.1
SEQ ID NO 38199
LENGTH: 72
                                                                                                                                                                                                                                                                                                                         MAP TO AL118522.7
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Best Local Similarity 18.8%; Pr
Matches 348; Conservative 240;
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                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Homo sapiens
FRATURE:
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US-10-341-434-236
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OTHER INFORMATION:
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APPLICANT: Renn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
IIILE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR ITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  515 --GDRKKSKGGR--------GGELQVWIKEAKNLTAAKAGGTSDSFVKGYLLDPMRNKA 562
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SE3 SKRKTPVWKKTLANPHYNHTFVYNGVRLEDLQHMCLELTVWDREPL--ASNDFLGGVRLGV 620
                                                                                -----LHG-----KKLDKKLDHCLP-----LHG-----KİS 485
                                                                                                                                                                                                                                                                                              749 LESK---PEPQVBLVVSRPIGDIPRIPDSTHAQLESSSSSFESQKWDRPSISVTSPMSPG 805
                                                                                                                                                                                                                                                                                                                                                                                                                          806 MLRDVPQFLSGQLSIKLWFDKVGHQLIVTILGAKDLPSREDGRPRNPYVKIYFLPDRSDK 865
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     866 NKRRIKIVKKILEPKWNOTPIYSPVHRREFRERMLBITLWDOARVREEESBFLGBILIEL 925
                                        629 IKDSGVDTCSSTTLNEEHSHSDKHPVTWQPSKDGDRLIGRILLNKRLKDGSVPRDSGAML 688
                                                                                                                                                                689 GLKVVGGKWTESGRLCAFITKVKKGSLADTVGHLRPGDEVLEWNGRLLQGATFEEVYNII 748
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CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR PILING DATE: 2000-02-04
PRIOR PILING DATE: 2000-02-04
PRIOR PILING DATE: 2000-03-26
PRIOR PLING DATE: 2000-06-26
PRIOR PILING DATE: 2000-06-03
PRIOR PILING DATE: 2000-06-03
PRIOR PILING DATE: 2000-06-03
PRIOR PILING DATE: 2000-06-03
PRIOR PILING DATE: 2000-09-27
PRIOR PILING DATE: 2001-01-04
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
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PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR PILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR PILING DATE: 2001-01-30
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PRIOR PILING DATE: 2001-01-30
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PRIOR APPLICATION NUMBER: PCT/US01/0670
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FILING DATE: 2000-09-21
APPLICATION NUMBER: US 09/608,408
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1113 SRSSERPDTNIAMESHPSIATGRSAPSPALSRSHPRTGSVQTSPSSTPGTGRRGUDDL 1172 1 1 1 1 1 1 1 1 1	US-08-800-644-94 Sequence 94, Application US/08800644 Patent No. 5-58975 GENERAL INFORMATION: APPLICANT: Red. in Grud APPLICANT: Chung, Soo-il TITLE OF INVENTION: Mehods of Using Same TITLE OF INVENTION: Mehods of Using Same TITLE OF INVENTION: Mehods of Using Same TITLE OF INVENTION: Mehods of Using Same TITLE OF INVENTION: Mehods of Using Same NUMBER OF SEQUENCES: 117 CORRESPONDENCE ADDRESS: ADDRESSER: Knobbe, Martens, Olson & Bear STREET: 620 Newport Center Drive, Sixteenth Floor CITY: Newport Beach CONTINE: US.A. ZIP: 92660 COMPUTER: IBM PC compatible COMPUTER: IBM P	# PRIOR APPLICATION NUMBER: # APPLICATION NUMBER: # ATLING DATE: 30-APR-1993 # ATTORNEY/AGENT INPORMATION: # RAME: Peditick, Michael F # REGISTRATION NUMBER: 36,799 # REFERENCE/DOCKET NUMBER: NIH054.001A # TELEPHONE: (714) 760-9502 # TELEPHONE: (714) 760-9502 # INPORMATION FOR SEQ ID NO: 94: # SEQUENCE CHARACTERISTICS: # LENGTH: 1898 amino acid # TYPE: amino acid # TYPE: amino acid # TYPE: TYPE: protein US-08-800-644-94	Query Match 3.7%; Score 307; DB 2; Length 1898, Best Local Similarity 17.4%; Pred. No. 4.6e-14; Matches 245; Conservative 213; Mismatches 514; Indels 434; Gaps 53;
264 BPORQREIQBEBEQILRKLIERQELRREGEBEGQOORILRREGQILRREGEBE 312 77 ITELVNINVIAPQORQPNIBREBOTKLHQDFEMYKEQVKRMGEBSQOOREQKGDAPTCG 133 8 13	RREQRILKRGEBERILGORILRS DETAINED FOR THE ACTUAL THE STANKING SERRICK STORM THE STANKING SERRICK STORM THE STANKING SERRICK STORM THE STANKING SERRICK STORM THE STANKING SERRICK STORM THE STANKING SERRICK STORM THE STANKING SERRICK STORM THE STANKING SERRICK STORM THE STANKING SERRICK STORM THE STANKING SERRICK SERVER SECRETARIES STANKING SERRICK SERVER SECRETARIES SERVER SERVER SECRETARIES SERVER SECRETARIES SERVER SECRETARIES SERVER SERVER SECRETARIES SERVER SERVER SECRETARIES SERVER SECRETARIES SERVER SECRETARIES SERVER SECRETARIES SERVER SECRETARIES SERVER SECRETARIES SERVER SECRETARIES SERVER SECRETARIES SERVER SECRETARIES SERVER SECRETARIES SERVER SECRETARIES SERVER SECRETARIES SERVER SECRETARIES SERVER SECRETARIES SERVER SECRETARIES SERVER SECRETARIES SERVER SECRITARIES SECRITARIES SECRITARIES SECRITARIES SECRITARIES SECRITARIES SECRITARIES SECRITARIES SECRITARIES SECR		1012BEQLIRBEREKRRRQSWERCYRKKDELQQBEBQL 1050 1053 HRGTRATGHYNTISRMDRHRVMDDHYSSDRDRDCEAADRQPYHRSRSTBQRFLIRRTTR 1112 1051 LREER

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Indels 434; Gaps 53;
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19 DPPPDEMPDLAHLTERS - NATHANDRONGERENGORDALANGORE -	DD 1051 LRER	RESULT 3 US-07-741-940-7 US-07-741-940-7 Sequence 7, Application US/07741940 Sequence 7, Application US/07741940 Sequence 7, Application US/07741940 Sequence 7, Application US/07741940 APPLICANT: ALBERTERN, HANS APPLICANT: CARLSON, MARSH APPLICANT: GRODEN, JOANNA APPLICANT: HEGGS, PHILIP J. APPLICANT: HANGE, PHILIP J. APPLICANT: NARKHAW, ALKXANDER F. APPLICANT: NARKHAW, ALKXANDER F. APPLICANT: THILVERIS, ANDREW APPLICANT: THILVERIS, ANDREW TITLE OF INVENTION: GENE IN COLORECTAL CANCER IN HUMANS TITLE OF INVENTION: GENE IN COLORECTAL CANCER IN HUMANS NUMBER OF SEQUENCES: 9 CORRESPONDENCES: 94 CORRESPONDENCES: 95 COURNESS: 1001 G Street, NW CITY: Washington STREET: 1001 G Street, NW CITY: Washington STREET: 105.	SMEmEUSDHWEMEM ER'YESSO
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Banner & Allegretti, LTD
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 PDRSDKNKRTKTVKKTLBPK-
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                                                                                                                           30 SHLTEBERKIILAVMDRQKKBERKEQSVLKIKERHKAQPTQWFPFSGITELVNNVLQPQQ
                                                                     Query Match 3.1%; Score 258.5; DB 1; Length 2842; Best Local Similarity 17.9%; Pred. No. 4.4e-10; Matches 304; Conservative 238; Mismatches 618; Indels 535; Gaps
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ORGANISM: Homo sapiens
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                                             1805 SÖNKÖSKKONLKNNSKOPNOKLPNNEDRVRGSPAPOSPHHYTPIRGTPYCFSRNDSLSSL 1864
                                                                                                                                  1077 HYSSDRDCEAAD-----PYHRSRSTE 1101
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                                                                                                BFRERMLEITLWDQARVREBESBFLGEILIELETALLDDEPHWYKLQTHDVSSLPLPR--
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APPLICANT: GRODEN, JOANNA
APPLICANT: GRODEN, JOANNA
APPLICANT: HEDGE, PHILIP J.
APPLICANT: HEDGE, PRILIP J.
APPLICANT: NINZLER, KENNETH
APPLICANT: NARKHAM, ALEXANDER F.
APPLICANT: HARKHAM, ALEXANDER F.
APPLICANT: THIJVERIS, ANDREM
TITLE OF INVENTION: INHERITED AND SOMATIC MUTATIONS OF APC
TITLE OF INVENTION: GENE IN COLORECTAL CANCER IN HUMANS
TITLE OF INVENTION: GENE IN COLORECTAL CANCER IN HUMANS
TITLE OF INVENTION: GENE IN COLORECTAL CANCER IN HUMANS
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562 LLDDSDDDIBILEBCIISAMPIKSSRKAKKAKTPAQTASKLPPFYARKPSQL-----PVYK 1615
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                             METMLKNDSLSSDQSESVRPPPRRPHKSKKGGKMRQVSLSSSBERL----ASTPEYTSC 568
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3.1%; Score 258.5; DB 1; Length 2842;
Best Local Similarity 17.9%; Pred. No. 4.4e-10;
Matches 304; Conservative 238; Mismatches 618; Indels 535;
                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION UNDER: US/08/289,548A
FILING DATE: 12-AUG-1994
CLASSIFICATION: 435
ATTONEX/AGENT INFORMATION:
NAME: REGISTRATION NUMBER: 32,141
REGISTRATION NUMBER: 32,141
REGISTRATION NUMBER: 32,141
TELEPHONE: 202-508-9100
TELEPHONE: 202-508-9299
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
                                                                                                                          ZIP: 20001-4598
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: BR PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
Street, NW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
STRANDEDNESS: single
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                                     Washington
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90 KOPNEKEPOTKLHQOPEMYKEQVKOMGEESQOOORQKGDAPYCGICHKTKFADGCGH	Db 1065 RQSRNQSTTYPVYTESTDDKHLKPQPHFGQQECVSFYRSRGANGSET 1111 Qy 147 NCSYCQTKFCARCGGRVSLRSNKVMWCMLCRKQQBILTKSGANFYNSGSNTLQQDDGKV 206 Qy 147 NCSYCQTKFCARCGGRVSLRSNKVMWCMLCRKQQBILTKSGANFYNSGSNTLQQDDGKV 206 1112 NRVGSNHGINQNVSQSLCQEDDYEDDKFTNYSERFSEREGHEE 1154	207 PRGLRNERAPQEKKAKLHEQPQPAPAGDLSVPAVEKGRAHGLTRQDTIKNGSGVKHQIA 	QY 267 SDMPSDRKRSPSVSRDQNRRYEQSEEREDYSQYVPSDGTMPRSPSDYADRRSQREPQFYE 326	Qy 327 EPGHLMYRDSRRRGHRHSKRTIVDD	Qy 356 SRDEYERÇRRESEYQARYRSDPNLARYPVKPQPYEBQMRIHABVSRARHERRHSDVSLAN 415 DD 1297 SANTLQIAEIKEKIGTRSAEDPVSEVPAVSQHPRIKSSRLQGS-SLSSESBARHKAVEFSS 1355	Qy 416 AELEDGRISLLRMDRPSRQRSVSERRAAMENQRSYSMERTREAQ 459	Qy 460GQSSYPQRISNHSPPTPRRSPIPLDRPDMRRADSLAKQHHLDPSSAVRKITKREK 513 Qy 1412 MVSGIISPSDLPDSPGQTMPPSRSKTPPPPPQTAQTKRR- 1450	Qy 514 METMLRNDSILSSDQSESVRPPPRPHKSKKGGKRRQVSLSSSEEELASTPEXTSC 568 1451	QY 569 D	Qy 596 VLSDSNTRSERQKGRAYYGGHSLEEDLEWSEPQIKDSGVDTCSS 639	Qy 640 TTLANEHSDKHPVTWQPSKDGDRLIGRILLANKRLKDGSVPRDSGAMLGL 690 1616 LLPSQNRLQPQKH-VSFTPGDDMPRVYCVBGTPINFSTATSLSDLTIESPPNELAAGEGV 1674	Qy 691 KVVGGRMTESGRLCAFITKVKKGSLADFVGHLRPGDEVLEWNGRLLQGATPEEVYNIILE 750 :	QY 751 SKPEPQVELVVSRPIGDIPRIPDSTHAQLESSSSSFESGRADRPSISVT 799 : ::	Qy 800 SPMSPGMLRDVPQFLSGQLSIKLMFDKVGHQLIVTILGAKDLPSREDGRPRNPYVKIYFL 859	QY 860 PDRSDKNKRIKIVKKILEPK	QY 894 EFRENLEITLWDQARVREESEFIGEILELETALLDDEPHWYKLQTHDVSSLPLPR 951	Qy 952 PSPYLPRRQL
QY 1347 SQLSQTEGGGKKLRSTVQRSTETGLAVEMRNWATRQASREST 1388	QY 1389DGSMNSYSS 1397 Db 2483 LSPGLPDMSLSTHSS 2497	RESULT 5 US-08-452-654-7 ; Sequence 7, Application US/08452654 ; Patent No. 5691454	GENERAL INFORMATION: APPLICANT: ALBERTSEN, HANS APPLICANT: ANAND, RAKESH APPLICANT: ANAND, RAKESH	GRODEN, GRODEN, GHEDGE, PI	· · · · ·	; TITLE OF INVENTION: INHERITED AND SOMATIC MUTATIONS OF APC ; TITLE OF INVENTION: GERE IN COLORECTAL CANCER IN HUMANS ; NUMBER OF SEQUENCES: 94 ; CORRESPONDENCE ADDRESS:	% c. ≅ ∵	; COUNTRY: USA ; ZIP: 20001-4598 ; COMPUTER READABLE FORM: ; MEDIUM TYPE: Floppy disk	; COMPUTER: IBM PC compatible ; OPERATING SYSTEM: PC-DOS/MS-DOS ; SOFTWARE: Patentin Release #1.0, Version #1.25 ; CURRENT APPLICATION DATA:	; APPLICATION NUMBER: US/08/452,654 ; FILING DATE: 25-MAY-1995 ; CLASSIFICATION: 536 ; PRIOR APPLICATION DATA:	; APPLICATION NUMBER: US 07/741,940 ; FILING DATE: 08-AUG-1991 ; ATTORNEY/AGENT INFORMATION: ; NAME: Kagan, Sarah A.	REGISTRATION NUMBER: 32,141 ; REPERENCE/DOCKET NUMBER: 1107.035574 ; TELECOMMUNICATION INFORMATION: ; TELEPHONE: 202-508-9100	74 A	; TYPR: amino acid ; STRANDEDNESS: single ; TOPOLOGY: linear ; MOLECULE TYPE: protein	OURCE : Ho SOURC	-654-7 atch 3.1%; Score 258.5; DB 1; Length 2842; atch 23.1%; Pred. No. 4.4e-10; 23.2.2.2.2.2.2.2.2.2.2.2.2.2.2.2.2.2.2.	MACCDES 304; CONSELVATIVE 238; MISMATCDES 618; INCELS 535; GAPS 59; QY 30 SHLTEEERKIILAVMDRQKKEEEKEQSVLKIKEEHKAQPTQWPPFSGITELVNNVLQPQQ 89 1 : : : : : : : : : : : :

PRIOR APPLICATION: «Unknown» PRIOR APPLICATION DATA: APPLICATION UNWESE: 108/289,548 FILING DATE: 12-AUG-1994 ATTORNEY/AGENT INFORMATION: NAME: RAGIO: Sarah A. REFERENCE/DOCKET NUMBER: 1107.46943 FELEFAM: 202-508-9100 TELEPAM: 202-508-9100 TELENGTHICATION INFORMATION: FELEFAM: 202-508-9299 INFORMATION FOR ERQ ID NO: 7: SEQUENCE CHARCITELSTICS: LENGTH: 2842 amino acide TYPE: mino acid FTARANDEDNESS: single NOLECTUA TYPE: protein ORIGINAL SOURCE: ORIGINAL SOURCE: MARGDIATE SOURCE: CLONE: APC SEQUENCE RESCRIPTION: SEQ ID NO: 7: SEQUENCE RESCRIPTION: SEQ ID NO: 7: SEQUENCE RESCRIPTION: SEQ ID NO: 7: US-08-449-731-7	Query Match 3.1%; Score 258.5; DB 4; Length 2842; Best Local Similarity 17.9%; Pred. No. 4.4e-10; Matches 304; Conservative 238; Mismatches 618; Indels 535; Gaps 69; Qy 30 SHLTESERKILLAVMDROKKEEEREQSVLKIKKEHKAQPTQWFPPSGITZLVMNVLQPQQ 89 Db	147 207 207 1155 267 267 1184 327 1237	Db 1297 \$ANTLQIAEIKEKIGTRSAEDPVSEVPAVSQHPRTKSSRLQGS-\$LSSESARHKAVERSS 1355 Qy 416 AELEDSRISLIRMDRPSRQRSVSERRAAMENQESYSHERTREAQ459 Db 1356 GAKSPĒKSGAQTPKSPPEHYVQETPLAFSRCTSVSSLDSFBSRJASSVQSEPCSG 1411 Cy 460GQSSYPQRTSNHSPPTPRRSPIPLDRPDWRRADSLRKQHHLDPSBAVRKTKREK 513 Db 1412 MVBGIISPSDLPDSPGQTWPPGRSKTPPP
988	Db 2319 PIOSPGRNŠISPGRNGIŠPPNKLŠQLPRTŠSPŠTAŠTKSSŠGGRŠ-TTŠPGRŽM8 2373 Qy 1287 GKNLTKSTSISGDMCSLEKUNGSQSDTAVGALGTSGKKRSSIGAKMVALVGLSRKSRSA 1346	LSPSLPDMSLSTHSS 2497 Application US/08449731 A13727 FORMATION: CARLSON, HANS ANAND, RAKESH CARLSON, MARY GRODEN, JOANNA HEDGE, PHILIP J. JOSLYN, GROFF KINZLER, KENNETH WARKHAM, ALEXANDER F. WARKAMURA, ALEXANDER F. NAKAMURA, ALEXANDER THLIVERIS, ANDREW	TITLE OF INVENTION: INHERITED AND SOMATIC MUTATIONS OF APC GENTE IN COLORECTAL CANCER IN HUMANS NUMBER OF SEQUENCES: 102 CORRESPONDENCE ADDRESS: ADDRESSER: Banner & Allegretti, LTD STREET: 1001 G Street, NM CITY: Mashington STREET: 1001 G Street, NM CITY: Mashington STREET: 20001-4598 COMPUTER: D.C. COUNTRY: USA INDICATION SYSTEM: PC-DOS/MS-DOS SOFTWARE: PRECOMPATION: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION NUMBER: US/08/449,731

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                                                                                                                                                                                                    1714 DNKAEEGDILAECINSAMPKGKSHKPFRVKKIMDQVQ-QASASSSAPNKNQLDGKKKKPT 1772
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -----DGVGVVSDYRHNG------RDLQSSTLSVPEQVMSSNHC 1020
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     1562 LLDDSDDDDIBILEBCIISAMPTKSSRKAKKPAQTASKLPPPVARKPSQL-----PVYK 1615
                                                                                                            1616 ILPSQNRLQPQKH-VSFTPGDDMPKVYCVEGTPINFSTATSLSDLTIESPPNELAAGEGV 1674
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                                                          640 TTLNEEHSHSDKHPVTWQPSKDGDRL--IGRILLLN-----KRLKDGSVPRDSGAMLGL 690
                                                                                                                                                                691 KVVGGKMTESGRLCAPITKVKKGSLADTVGHLRPGDEVLEWNGRLLQGATFEEVYNIILE 750
                                                                                                                                                                                                                                                                          751 SKPEPQVELVV----SRPIGD-----IPRIPDSTHAQLESSSSFESQKMDRPSISVT 799
                                                                                                                                                                                                                                                                                                                                                                                800 SPMSPGMLRDVPQFLSGQLSIKLMPDKVGHQLIVTILGAXOLPSRBDGRPRNPYVKIYFL 859
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1012 NHMDDNDGELDTPINYSLKYSDEQ----LNSGRQSPSQNERWARPKHIE--DEIRQSEQ 1065
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: INHERITED AND SCHATIC MUTATIONS OF APC
TITLE OF INVENTION: GENE IN COLORECTAL CANCER IN HUMANS
MUDBER OF SEQUENCES: 102
CORRESPONDENCE ADDRESS:
ADDRESSEE: BANNET & Witcoff, Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: FLOPEY GIBE
COMPUTER: FLOPEY GIBE
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/452,655B
FILING DATE: 25-MAY-1995
CLIASSIPICATION DATA:
APPLICATION NUMBER: US 08/289,548
FILING DATE: 12-AMG-1994
PRICE APPLICATION DATA:
APPLICATION NUMBER: US 07/741,940
FILING DATE: 08-AUG-1991
ATTORNEY/AGENT INFORMATION:
APPLICATION NUMBER: 32,141
REGISTRATION NUMBER: 32,141
REGISTRATION NUMBER: 32,141
REGISTRATION NUMBER: 32,141
RELEPHONE: 202-508-9100
TELEFRAN: 202-508-9299
INFORMATION POR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LEMETRIE COMMUNER: 202-508-3299
INFORMATION POR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
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ADDRESSER: Banner & Witcoff, Ltd.
STREF: 1001 G Street, NW
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20001-4598
COMPUTER READABLE FORM:
WEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                            APPLICANT: CARLSON, MARY
APPLICANT: GRODEN, JOANNA
APPLICANT: HEDGE, PHILLP J.
APPLICANT: JOSLYN, GROFF
APPLICANT: KINZLER, KENNETH
APPLICANT: MARKHAM, ALEXANDER F.
APPLICANT: NAKANURA, YUSUKE
APPLICANT: THLIVERIS, ANDREW
Sequence 2, Application US/08452655B
Patent No. 5783666
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1806 SDNKOSKKONLKANSKOPNOKLPNNEDRVRGSPAFDSPHHYTPIRGTPYCFSRNDSLSSL 1865
                                                                                                                                                                                                                                                                                      1866 DFDDDDVDLSR-EKAELEKAKENKESEAKVTSHTELTSNQQSANKTQA--LAKQPINKGQ 1922
                                                                                                                                                                                                                                                                                                                                                            ------DGVGVVSDYRHNG------RDLQSSTLSVPRQVMSSNHC 1020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1021 SPSGSPHRVD---VIGRIRSWSPSAPPPORRVEQGHRGIRATGHYNTISRWD-RHRVMDD 1076
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                                                         751 SKPEPQVELVV----SRPIGD-----IPRIPDSTHAQLESSSSSFESQRADRPSISVT 799
                                                                                                                                                                                                                                                                                                                                        PSPYLPRRQL-----HGESPTRRLQR-----SKRISDSEVSDYDCE---- 987
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                                                                                                                                                                                               860 PDRSDKNKRRIKIVKKTLEPK-------RNQIFIYSPVH------RR
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Patent No. 6114124
GENERAL INFORMATION:
APPLICANT: ALBERTSEN, HANS
APPLICANT: ANADY, RAKESH
APPLICANT: CARLSON, MARY
APPLICANT: GRODEN, JOANNA
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US-08-450-582-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           327 EPGHLNYRDSNRRGHRHSKE----YIVDD-------------EDVE 355
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                                                                                                                                                                                                                                                                                    Query Match
3.1%; Score 258.5; DB 1; Length 2843;
Best Local Similarity 17.9%; Pred. No. 4.4e-10;
Matches 304; Conservative 238; Mismatches 618; Indels 535;
32,141
ab: 1107.49964
     REGISTRATION NUMBER: 32,141
REFERENCE/DOCKET NUMBER: 110
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-508-9100
TELEFAX: 202-508-9299
                                                                                      INFORMATION FOR SEC 1D NO: 7: SEQUENCE CHARACTERISTICS: LENGTH: 2843 amino acids TYPE: amino acid STRANDEDNESS: single TOPOLOGY: linear MOLECULE TYPE: protein HYPOTHETICAL: YES
                                                                                                                                                                                                                                   ANTI-SENSE: NO
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                                                                                                                                                                                                            1357 GAKBPSKSGAQTPKSPPRHYVQETPLMFSRCTSVS----SLDSFBSRSIASSVQSEPCSG
                                                                                                                                                                                                                                                                                                           413 MVSGIISPSDLPDSPGCTMPPSRSKTPPP------PPQTA--CTKRE-
                                                                            SRDEYERORREERY QARYRSDPNLARY PVKPOPYEROMRIHAEVERARHERRHSDVSLAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | : | : | : | : | : | NGSNHGINQNVSQSLC----QEDDYEDDKPTNYSERYBEBEQHEB-- 1155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1066 RQSRNQS-----TTYPVYTESTDDKHLKPQPHPGQQE-----CVSPYRSRGANGSET 1112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                90 KOPNEKEPOTKLHOOFEMYKEQVKKMGEESQQ---QQEQKGDAPTCGICHKTKFADGCGH 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               147 NCSYCQTKFCARCGGRVSLRSNKVMWYCNLCRKQQBILTKSGAWFYNSGSNTLQQPDQKV 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                207 PRGLRNERAPQEKKAKLHEQPQPQGAPGDLSVPAVEKGRAHGLTRQDTIKNGSGVKHQIA 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SDMPSDRKRSPSVSRDQNRRYEQSBEREDYSQYVPSDGTMPRSPSDYADRRSQREPQFYE 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BPGHLNYRDSNRRGHRHSKE----YIVDD-----------EDVE 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30 SHLTERERKIILAVMDRQKKEBEKEQSVLKIKEEHKAQPTQWPPFSGITELVNNVLQPQQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
3.1%; Score 258.5; DB 3; Length 2843;
Best Local Similarity 17.9%; Pred. No. 4.4e-10;
Matches 304; Conservative 238; Mismatches 618; Indels 535;
APPLICANT: HEDGE, PHILIP J.
APPLICANT: JOSLYN, GEOFF
APPLICANT: KINZLER, KENNETH
APPLICANT: MARKHAM, ALEXANDER F.
APPLICANT: MARKHAM, ALEXANDER F.
APPLICANT: THALIVERIS, ANDREW
TITLE OF INVENTION: INHERITED AND SOMATIC MUTATIONS OF APC
TITLE OF INVENTION: GENE IN COLORECTAL CANCER IN HUMANS
CORRESPONDENCE: 102
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                       COUNTRY: U.C.

ZIP: 2001-4598

ZIP: 2001-4598

COMPUTER READBLE PORN:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/08/450,582
PILING DATE: CLASSIPICATION NUMBER: US/08/450,582
PILING DATE: 22-MAY-1995
APPLICATION NUMBER: US 08/25,655
FILING DATE: 12-MAY-1995
APPLICATION NUMBER: US 08/29,548
FILING DATE: 12-MAJ-1994
PRICH AGENT NUMBER: US 07/741,940
FILING DATE: 08-MAJ-1991
ATTORNEY/AGENT INFORMATION:
NAME: KAGAN, SATSH A.
REGISTRATION NUMBER: 32,141
REFERENCE/DOCKET NUMBER: 1107,49964
TELERDHONE: 202-500-9100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -----EERPTNYSIKYNEEKRHVDQPIDYSL-----
                                                                                                                                                                                                                                                ADDRESSEE: Banner & Witcoff, Ltd.
STREET: 1001 G Street, NW
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2843 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           202-508-9299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-450-582-2
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1357 GAKSPSKSGAQTPKSPEHYVQETPLMFSRCTSVS----SLDSFESRSIASSYQSEPCSG 1412
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1617 LLPSQNRLQPQKH-VSFTPGDDMPRVYCVEGTPINPSTATSLSDLTIRSPPNELAAGEGV 1675
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1676 R--GG--AQSG------EPEKRDTIPTEG--RSTDEA------QGGKTSSVTIPELD 1714
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1715 DNKAEBGDILAECINSAMPKGKSHKPPRVKKIMDQVQ-QASASSSAPNKNQLDGKKKKPT 1773
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1113 N------RUGSNHGINQNVSQSLC----QEDDYEDDKPTNYSERYSEEBQHEE-- 1155
                                                                                                                                                                                                                                                                                                                                                                                                                1012 NEMDDNDGKLDTPINYSLKYSDEQ----LNSGRQBPSQNKRWARPKHIIE--DKIKQSKQ 1065
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             267 SDMPSDRKRSPSVSRDQNRRYEQSERREDYSQYVPSDGTMPRSPSDYADRRSQREPQFYE 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               327 BPGHLNYRDSNRRGHRHSKE----YIVDD-------------BDVB 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 356 SRDEYERQRRESEYQARYRSDPNLARYPVKPQPYERGMRIHAEVSRARHERRHSDVSLAN 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      416 AELEDSRISLIRMDRP-----4 SRQRSVSERRAAMENQRSYSMERTREAQ---- 459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        460 -----GOSSYPORTSNHSPPTPRRSPIPLDRPDMRRADSLRKGHHLDPSSAVRKTKREK 513
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            691 KVVGGKMTESGRLCAFITKVKKGSLADTVGHLRPGDEVLEMNGRLLQGATFEEVFNIILE 750
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               751 SKPEPQVELVV----SRPIGD-----IPRIPDSTHAQLESSSSFESQKWDRPSISVT 799
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  90 KQPNEKEPQTKCHQQPEMYKEQVKKMGEESQQ----QQRQKGDAPTCGICHKTKPADGCGH 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         207 PRGLRNEEAPQEKKAKILHEQPQFQGAPGDLSVPAVEKGRAHGLTRQDTIKNGSGVKHQIA 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 596 VLSDSN------TRSERQKKRMYYGGHSLEEDLEMSEPQIKDSGVDTCSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             514 METWLRNDSLSSDQSESVRPPPRRPHKSKKGGRMRQVSLSSSBEBEL----ASTPEYTSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    147 NCSYCQTKFCARCGGRVSLRSNKVMWYCNLCRKQQBILTKBGAWFYNSGSWTLQQPDQKV
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                                                                                                                                                                                                                                                                                                                                                                30 SHLTEBERKIILAVMDRQKGEBEKBQSVLKIKBEHKAQPTQWPPFSGITELVNNVLQPQQ
                                                                                                                                                                                                                                                              Query Match 3.1%; Score 258.5; DB 3; Length 2843; Best Local Similarity 17.9%; Pred. No. 4.4e-10; Matches 304; Conservative 238; Mismatches 618; Indels 535; Gaps
SEQUENCE CHARACTERISTICS:
LENGTH: 2843 amino acida
                                                  TYPE: amino acid
STRANDENNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
                                                                                                                                                                                 ; ANTI-SENSE: NO
US-08-450-582-7
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                                                          1175 KGTLERSAMDIEERNROMKLNKYKOVAGSDPRLEODYHSKYRSG----WDPHRGAD---- 1226
                                                                                                                                                         1227 TVSTKSSDSDVSDVSDVSRVSRTSSASRPSSTSYMSVQSERPRGNRKISVFTSKMQNRQMGVS 1286
                                                                                                                                                                                         2320 PIGSPGRNSISPGRNGISPPNTLSQLPRTSSPSTASTKSSGSGRAS-TTS--PGRQM--S 2374
                                                                                                                                                                                                                                                              1287 GKNLTKSTSISGDMCSLEKNDGSQSDTAVGALGTSGKKRRSSIGAKWVAIVGLSRKSRSA 1346
                                                                                                                                                                                                                                                                                                1347 SQLSQTRGGGKKL-----RSTVQRSTBTGLAVEMRNWHTRQASREST---- 1388
                                                                                                                                                                                                                                                                                                                                                                                                                  2424 SSGSESDRSERPVLVROSTFIKEAPSPTLRRKLEESASFESLSPSSRPASPTRSQAQTPV 2483
       2216 PLQANMPSISRGRIMIHIPGVRNSSSSTSPVSKKGPPLKTPASKSPSEG----QTATTSP 2271
                                                                                                  2272 RGAKPSVKSELSPVARQT----SQIGGSS-----KAPSRSGSRDSTPSRPAQQPLSR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: ALBERTSEN, HANS
APPLICANT: ANAD, RAKESH
APPLICANT: CALLSON, MARY
APPLICANT: GRODEN, JOANNA
APPLICANT: GRODEN, JOANNA
APPLICANT: HEDGE, PHILIP J.
APPLICANT: GRODEN, GROPEP
APPLICANT: KENNETH
APPLICANT: KENNETH
APPLICANT: MARKHAM, ALEXANDER F.
APPLICANT: MARKHAM, ALEXANDER F.
APPLICANT: THILVERIS, ANDREW
TITLE OF INVENTION: INHERITED AND SOMATIC MITATIONS OF APC
TITLE OF INVENTION: GENET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/450,582
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/452,655
FILING DATE: 25-MAY-1995
APPLICATION NUMBER: US 08/289,548
FILING DATE: 12-MG-1994
FRIOR APPLICATION NUMBER: US 07/741,940
FILING DATE: 08-AUG-1991
APPLICATION NUMBER: US 07/741,940
FILING DATE: 08-AUG-1991
ATTORNEY/AGENT INPORMATION:
NAME: KAGAI, 3arah A.
REGISTRATION NUMBER: 32,141
REFERENCE/DOCKET NUMBER: 1107,49964
TELECOMMUNICATION INPORMATION:
TELECOMMUNICATION INPORMATION:
TELECOMMUNICATION INPORMATION:
TELECOMMUNICATION INPORMATION:
TELECOMMUNICATION INPORMATION:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 7, Application US/08450582
Patent No. 6114124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2484 LSPSLPDMSLSTHSS 2498
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: 1001 G Street, NW CITY: Washington STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 202-508-9299
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: USA
ZIP: 20001-4598
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 10
US-08-450-582-7
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COMPOTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFWARR: FRSIESC for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/821,355A
FILING DATE: 20-MAR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Regan, Sarah A
REGISTRATION NUMBER: 32,145
REFRENCE/DOCKET NUMBER: 1107
TELEPCOMMUNICATION INPORMATION:
TELEPTONE: 202-508-9100
TELEX: 97430 BMB UT
INPORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
                                      F: 1001 G Street, N.W
Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: No. 5851775e
                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                       FILING DATE: 20-MAR-19
CLASSIFFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
CORRESPONDENCE ADDRESS:
ADDRESSEE: Banner &
                                                                                                                                          COMPUTER READABLE FORM:
                                    STREET: 100
CITY: Washi
STATE: DC
COUNTRY: US
ZIP: 20001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-821-355A-7
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                                                                                                                                                                                                                                                                                                                                                        ------DGVGVVSDYRHNG------RDLQSSTLSVPEQVMSSNHC 1020
                                                                                                                                                                                                                                                                                                                                                                                                                                        1021 SPSGSPHRVD---VIGRTRSWSPSAPPPQRRVBQHRGTRATGHYNTISRMD-RHRVMDD 1076
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2043 ISSAMPKKKKPSRLKGDNEKHSP-----RNM-GGILGEDLTLDLKDİQRPÖSEHGLSPD 2095
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                                                            SÖNKÖSKKÖNLKANSKOFNDKLPANTEDRVRGSPAFDSPHHYTPIEGTPYCFSRNDSLSSL 1865
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                                                                                                     860 PDRSDKNKRRIKIVKKTLEPK-----RHQTFIYSPVH-----RR 893
                                                                                                                                                                                   BFRERMLEITLMDOARVREESSEFLGEILIELETALLDDEPHWYKLGTHDVSSLPLPR-- 951
                                                                                                                                                                                                                                                                        PSPYLPRRQL-----HGESPTRRLQR-----SKRISDSEVSDYDCE---- 987
                     SPMSPGMLRDVPQFL8GQL61KLMFDKVGHQLIVT1LGAKDLPSREDGRPRNPYVK1YFL 859
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Patent No. 5851775
GENERAL INFORMATION:
APPLICANT: Barker, Nick
APPLICANT: Clevers, Hans
APPLICANT: Korinek, Vladimir
APPLICANT: Morin, Patrice
APPLICANT: Morin, Patrice
APPLICANT: Vogelstein, Bert
APPLICANT: Vogelstein, Bert
APPLICANT: Vogelstein, Bert
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                                                                                                                                                                                                                                                                              147 NCSYCOTKFCARCGGRVSLRSNKVMWVCNLCRKQQBILITKSGAMFYNSGSNTLQQPDQKV
                                                                                             30 SHLTEBERKIILAVMDRQKKEBEKEQSVLKIKEHKAQPTQMFPFSGITELVNNVLQPQQ
Query Match 3.1%; Score 258.5; DB 2; Length 2973; Best Local Similarity 17.9%; Pred. No. 4.7e-10; Matches 304; Conservative 238; Mismatches 618; Indels 535; Gaps
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Beta Catenin, TCF-4, and APC Interact to Prevent Cancer

APPLICANT: Kinzler, Kenneth APPLICANT: Vogelstein, Bert APPLICANT: Sparks, Andrew TITLE OF INVENTION: Beta Cater TITLE OF INVENTION: Interact I NUMBER OF SEQUENCES: 11

Db 2375 QONLTKQTGLSKNASSIPRSESASKGLNQMNNGANGANKKVELSRMSSTK 2423 Qy	RESULT 12 US-09-003-687A-7 Sequence 7, Application US/09003687A Sequence 7, Application US/09003687A Sequence 7, S9860 Patent No. 599860 Sequence 7, Application: APPLICANT: Barker, Nick APPLICANT: Rorinek, Vladimir APPLICANT: Korinek, Vladimir APPLICANT: Morin, Patrice SAPLICANT: Morin, Patrice SAPLICANT: Morin, Patrice SAPLICANT: Morin, Patrice	APPLICANT: Sparks, Andrew APPLICANT: Sparks, Andrew TITLE OF INVENTION: Beta Catenin, TCF-4, and APC TITLE OF INVENTION: Interact to Prevent Cancer NUMBER OF SEQUENCES: 11 CORRESPONDENCE ADDRESS: ADDRESSER: Banner & Witcoff, Ltd. STREET: 1001 G Street, N.W. CITY: Washington STATE: DC COUNTRY: USA ZIP: 2001 COMPUTER READABLE FORM:	MEDIUM TYPR: Diskette COMPUTER: IDA COMPATIBLE OPERATING SYSTEM DOS SOFTWARE: FastSEQ for Windows Version 2.0 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/003,687A FILING DATE: CLASSIPICATION: PRIOR APPLICATION: APPLICATION NUMBER: 08/821,355 FILING DATE: 20-MAR-1997 ATTORNEY/AGENT INPORMATION:	NAME: REGISTRATION NUMBER: 32,145 REGISTRATION NUMBER: 32,145 REFFERENCE/DOCKET NUMBER: 1107.05064 TELECOMMUNICATION INFORMATION: TELEPHONE: 202-508-9100 TELEPHONE: 202-508-9299 TELEX: 97430 BMB UT INFORMATION POR SEQ ID NO: 7: SEQUENCE CHARACTERISTICS: LENGTH: 2973 amino acids TYPE: amino acids TYPE: amino acids TYPE: amino acids TYPE: amino acids TYPE: amino acids TYPE: amino acids TYPE: amino acids TYPE: amino acids TYPE: amino acids TYPE: amino acids TYPE: amino acids TYPE: amino acids TYPE: amino acids TYPE: amino acids TYPE: amino acids TYPE: amino acids TYPE: TYPE: NO: 5998600e	US-09-003-687A-7 3.1%; Score 258.5; DB 2; Length 2973; Query Match
	PVYK PVYK MLGL	1676 RGGAQSGEPPEKEDTIPTEGKSTDEAQGGKISSVTIPELD 1714 751 SKDEDQVELVVSRPIGDIPRIPDSTHAQLESSSSSFESGRONDRFSISVT 799 1715 DNKAERGDILAECINSAMPRGKSHKPPRVKKIMDQVQ-QASASSSAPNKNQLDGKKKRPT 1773 800 SPMSPGMLRDVPQPLSGQLSIKLMFDKVGHQLIVTILGAKDLPSREDGRPRNPYVKIYFI 859 1774 SPVKPIPQNTSYRTKV	894 EFRERMLEITLWDQARVREBESBFLGEILIELETALLDDBPHWYKLQTHDVSSLPLPR 951 1866 DFDDDDVDLSR-EKAELRKAKENKESEAKYTSHTELTSNQQSANKTQAIAKQPINRGQ 1922 952 PSPYLPRRQLHGESPTRLQRSKRISDSEVSDYDCE 987 1923 PKPILGKQSTFPQSSKDIPDRGAATDEKLGNPAIENTPVCFSHNSSLSSLSDIDQERNNK 1982 968DGVGVVSDYRHNG	1021 SPSGSPHRVDVIGRTRSWSPAPPPQRNVEQGHRGTRATGHYNTISRWD-RHRVWDD 1076	2216 PLOANMPSISRGRTMIHIPGVRNSSSTSPVSKKGPPLKTPASKSPSRGQTATTSP 2271 1175 KGTLERSAMDIBERNRQMKLANKYKQVAGSDPRLRQDYHSKYRSGMDPHRGAD 1226 1272 RGAKPSVKSELSPVARQTSQIGGSSKAPSRSGSRDSTPSRFAQQPLSR 2319 1227 TVSTKSSDSDVSDVSAVSRTSSASRFSSTSYMSVQSERPRGRIKISVFTSKMQNRQMGVS 1286 12320 PIQSPGRNSISPGRNKLSQLPRTSSPSTASTKSSGSGRNS-YTSPGRQMS 2374 1287 GKNLTKSTSISGDMCSLEKNDGSQSDTAVGALGTSGKKRRSSIGAKWVALVGLSRKSRSA 1346 1287 GKNLTKSTSISGDMCSLEKNDGSQSDTAVGALGTSGKKRRSSIGAKWVALVGLSRKSRSA 1346 1287 GKNLTKSTSISGDMCSLEKNDGSQSDTAVGALGTSGKKRRSSIGAKWVALVGLSRKSRSA 1346 1287 GKNLTKSTSISGDMCSLEKNDGSQSDTAVGALGTSGKKRRSSIGAKWVALVGLSRKSRSA 1346

PPPCRNVEGGHRGTRATGH	12320 198PGRN31SPGRN31SPPNKLSQ1PRTSSPSTASTKSSGSGRMS-YT8PGRQMS 2374 QY	RESULT 13 US-09-136-605-7 IS-09-136-605-7 Sequence 7, Application US/09136605A Fatent No. 6140052 GENERAL INFORMATION: APPLICANT: He, Tong-Chuan APPLICANT: Ho, Tong-Chuan APPLICANT: Wogelstein, Bert TITLE OF INVENTION: Bera Catenin, TCF-4, and APC Interact to TITLE OF INVENTION: Prevent Cancer FILE OF INVENTION: Prevent Cancer FILE OF INVENTION: 1107-75741 CURRENT APPLICATION NUMBER: US/09/136,605A CURRENT APPLICATION NUMBER: US/09/1355 RARLIER APPLICATION NUMBER: 1997-03-20 RARLIER APPLICATION NUMBER: 09/003,687	inducer Filth Date: 1938-01-06 inducer Filth Date: 1938-01-06 inducer Filth Date: 1938-01-06 inducer Filth Date: 1938-01-06 inducer Filth Date: 1939 inducer Match Ducery Match Best Local Similarity 17.9%; Pred. No. 4.7e-10; Matches 304; Conservative 238; Mismatches 618; Indels 535; Gaps 69; Qy 30 SHITESERKIILAVWDRQKKEEKEQSVÄKIKERHKAQPTGMFPFSGITELYNNVLQPQ 89 inducer Filth Date: 1
· ·	16 AELEDSEITSLIANDRPSRORGYSERRAAMENGRSYSMERTERAQ	VLSDSNTRSEROKCRMYYGGHSLEEDLEWSEPQIKDSGVDTCSS	174 SPWRP

Qy 1021 SPSGSPHRVDVIGRTRSWSPSAPPPQRNVEQG	DD 2043 ISSAMPKKKFPSRLKGDNEKHSPRNM-OG	Cy 1077 HYSSDRDRDCEAADRQ	DD 2096 SENFOWKAIQEGANSIVSSIHQAAAAACLSRQASS	1102	DD 2156 RKPFTSNKGFRILKPGEKSTLETKKIESESKGIKG OV 1123 -LAMESMPSLATGESAPDSPALSESHPRTGSV	2216	Qy 1175 KGTLERSAMDIEERNRGMKLNKYKQVAGSDPRLEQ	1227	2320	Qy 1287 GKNLTKSTSISGDMCSLEKNDGSQSDTAVGALGTS	Oy 1347 SQLSQTEGGGRGRSTVQRSTET	2424 SSGSESDRSERPVLVROSTFIKEAPSPT	Qy 1389DGSMNSYSS 1397	RESULT 14	US-U/-/41-940-2 ; Sequence 2, Application US/07741940 ; Patent No. 5352775	GENERAL INFORMATION: APPLICANT: ALBERTSEN, HANS APPLICANT: ANAND, RAKESH	GRODEN, HEDGE, F	JOSLYN, GE KINZLER, F MARKHAM, A	, APPLICANT: NAKAMURA, YUSUKR , APPLICANT: THILVERIS, ANDREW : TITLE OF INVENTION: INHERITED AND SOWATIC W	OF INVENTION: GENE IN COLORE R OF SEQUENCES: 94 SPONDENCE ADDRESS:	ADDRESSEE: Banner, Birch, McKie & Beckett STREET: 1001 G Street, NN	STATE: D.C. COUNTRY: U.S.A.	; ZIP: 20001-4598 ; COMPUTER READABLE FORM: ; MEDIUM TYPE: Floppy disk	COMPUTER: IBM PC compatible COMPUTER: IBM PC compatible COMPUTER: Patentin Release #1.0, Version	APPLICATION NUMBER: US/07/741,940 ; FILING DATE: 19920109	; CLASSIFICATION: 435 ; ATTORNEY/AGENT INFORMATION: ; NAME: Kagan, Sarah A.
	NCSYCOTKFCARCGGRVSLASNKVMWVCNLCRKQQBILITKSGAMFYNSGSNTLQQBDQKV	LIIS NKVGSNHGINQNVSQSLCQEDDIEDDARINEEREEGHEEF- IIOS	PRGLENKERAPURKKAKTHEOPYPGGAPGOLSVPAVEKGARAHGLIKUDITIKNGSGVKHQIA		: : : : :	327 EPGHLNYRDSNRRGHRHSKEYIVDD		1298 SANTLQIABIKEKIGTRSAEDPVSEVPAVSQHPRIKSSRLQGS-SLSSESARHKAVBFSS 1356	416 AELEDSRISLLRMDRPSRQRSVSERRAAMENQRSYSMERTREAQ 459	PRRSPIPLORPOMRRADSLRKQHHLOPSSAVRTTKREK	1413 WVSGIISPSDLFDSPGQTMPPSRSKTPPP	-GPKQAAVNAAVQRVQLPDADTLIHFATESTPDGFSC	569 D	TRSEROKKRMYYGGHSLEEDLEWSEPQIKDSGVDTCSS		640 TTLNBEHSHSDKHPVTMQPSKDGDRLIGRILLNKRLKDGSVPRDSGAMLGL 690 1617 LLPSQNRLQPQKH-VSFTPGDDMPRVYCVBGTPINFSTATSLSDLTIESPPNELAAGRGV 1675		1676 RGGAQSGEPEKKDTIPTEGRSTDRAQGGKTSSVTIPELD 1714 751 SKPEPQVELVVSRPIGDIPRIPDSTHAQLESSSSFRSQKWDRPSISVT 799	1715 DNKABEGDILABCINSAMPKGKSHKPFRVKKIMDQVQ-QASASSSAFNKNQLDGKKKKFT 1773	800 SPMSPGMLRDVPQFLSGQLSIKLMPDKVGHQLIVTILGAKDLPSREDGRPRNPYVKIYFL 859	WNQTFIX	1806 SDNIDSKYQMLKNNSKDFNDKLPNNEDRVRGSFAFDSPHHYTPIEGTPYCFSRNDSLSSL 1865	894 BFRERMLETTLMDQARVREERSEFLGEILIELETALLIDDEPHWYKLGTHDVSSLPLPR 951 : : ::: : : : : : 1		1923 FALL LUCKUSTIFFQSSALL FURGAATUEKLÜNFALENIFVCFSHNSSLSSLSLLUCKENNNA. 1902 988DGVGVVSDYRHNGRDLOSSTLSVPEOVNSSNHC 1020	ENBPIKETEPPDSQGEPSKPQASGYAPKSFHVEDTPVCFSRNSSLSSLSIDSBDDLLQEC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VLSDSN-------TRSERQKKRMYYGGHSLEEDLEWSEPQIKDSGVDTCSS 639
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                                                                                                                                                                                       Query Match
3.0%; Score 250.5; DB 1; Length 2843;
Best Local Similarity 18.0%; Pred. No. 1.8e-09;
Matches 305; Conservative 235; Mismatches 620; Indels 535;
 32,141
KR: 1107.035574
REGISTRATION NUMBER: 32,141
REFERENCE/POCKET NUMBER: 1107
TELECOMMULTATION INFORMATION:
TELEPHONE: 202-508-9100
INFORMATION FOR SEQ 1D NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                   LENGTH: 2843 amino acids TYPE: AMINO ACID
                                                                                                                           TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                            US-07-741-940-2
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1774 SPVKP-----IPQNTEXPIRV-------RKNADSKNILMAERVF 1805
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1983 ENEPIKETEPPDSQGEPSKTPQASGTAPKSFHVEDTPVCFSKNSSLSSLGIDSEDDLIQEC 2042
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DNKAERGDILARCINSAMPKGKSHKPFRVKKIMDQVQ-QASASSSAPNKNQLDGKKKKPT 1773
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                                                                   SPMSPGMLRDVPQFLSGQLSIKLMPDKVGHQLIVTILGAKDLPSREDGRPRNPYVKIYFL 859
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Patent No. 5648212
GENERAL INFORMATION:
APPLICANT: ALBERTSEN, HANS
APPLICANT: ANAND, RAKESH
APPLICANT: CARLSON, WARY
APPLICANT: GRODEN, JOANNA
APPLICANT: GRODEN, JOANNA
APPLICANT: GRODEN, GEOFF
APPLICANT: ARNIETH
APPLICANT: KINZLER, KENNETH
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1983 ENRPIKETEPPDSQGEPSKPQASGYAPKSFHVEDTPVCFSRNSSLSSISIDSEDDLLQBC 2042
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                                                                                   1413 MVSGIISPSDLPDSPGQTMPPSRSKTPPP--------PPQTA--QTKKE-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 3.0%; Score 250.5; DB 1; Length 2843; Best Local Similarity 18.0%; Pred. No. 1.8e-09; Matches 305; Conservative 235; Mismatches 620; Indels 535;
APPLICANT: MARKHAM, ALEXANDER F.
APPLICANT: NAKAMURA, YUSUKE
APPLICANT: THLIVERIS, ANDREW
TITLE OF INVENTION: INHERITED AND SOMATIC MUTATIONS OF APC
TITLE OF INVENTION: GENE IN COLORECTAL CANCER IN HUMANS
NUMBER OF SEQUENCES: 102
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                        COUNTRY: 1001 G Street, NW
STREET: 1001 G Street, NW
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20001-4598
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PEN PC compatible
COMPUTER: PEN PC compatible
COMPUTER: PEN PC compatible
COMPUTER: PEN PC compatible
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COMPUTER: PEN PC compatible
COMPUTER: PEN PC compatible
COMPUTER: PEN PC compatible
COMPUTER: 12-AUG-1994
CLESSIFICATION: A35
ATTORNEY/AGENT INFORMATION:
REFERENCE/DOCKET NUMBER: 1107-46943
TELEFORMUNICATION INFORMATION:
TELEFORMUNICATION INFORMATION:
TELEFORM COMPATION COMPATION:
TELEFORM COMPATION COMPATION:
TELEFORMATION POR SEQ 1D NO: 2:
SEQUENCE CHARACTERISTICS:
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TYPE: amino acid
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MOLECULE TYPE: protein
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us-09-617-099b-1.rai

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Search completed: December 12, 2003, 07:21:57 Job time : 63 secs
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Copyright (c) 1993 - 2003 Compugen Ltd.
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1107863 1107863 segs, 158726573 residues Searched:

Potal number of hits satisfying chosen parameters:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Minimum DB seq length: 0 Maximum DB seq length: 200000000

/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA2003.DAT /geneseqp-embl/AA1992.DAT geneseqp-embl/AA1995. A Geneseq 19Jun03:*
| /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1980. /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1984. /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1985. /SIDS1/gcgdata/geneseg, /SIDS1/gcgdata/geneseq /SIDS1/ /SIDS1/ /SIDS1/ SIDS1, /SIDS1 Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		*			SUMMARIES	
Result No.	Score		Query Match Length DB	90	a	Description
-	8285	•	:		AAB73488	Mouse Rim2, a r
71	2215	26.7	427	23	ABP63531	KIAA 0751 PDZ d
m	1586.5			19	AAW29640	Human secreted
4	1015.5			77	AAB34848	Human secreted
ស	1010.5				AAB34847	Gene 46 human a
9	989				ABB63174	Drosophila mela
7	624	7.5			AAB34849	Gene 46 human s
œ	569.5	6.9		55	ABB15089	Human nervous a
σ	266	9			AAB34850	Human secreted

KIAA 0751 PDZ doma Buman ORFX ORF489 KIAA 0751 PDZ doma FDZ encoded domain FDZ domain. Howo FDZ domain. Howo	man tri ophila ophila		lla me lla me lla me lver p spride #996		Human ORFX ORF2255 Human secretory po Drosophila melanog Novel human protei Drosophila melanog Drosophila melanog Human polypeptide
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ABP63532 AAB40725 ABP63179 AAB55848 AAB558049	AAY30795 ABB60327 ABB60291	ABB71160 ABB66948 ABR47592 ABR47604	ABB58724 ABB71141 ABP69569 ABG48336 ABB28314	ABB18950 AAM54270 AAM66665 AAM14533 AAM26950 AAM02259	AAB42491 ABP75873 ABB59050 ABB97332 ABB63166 ABB70936
ABP6353 AAB4072 ABP6317 AAB5584 AAB5763 AAB5804	AAY3079 ABB6032 ABB6029 ABB6577	ABB7116 ABB6694 ABR47594 ABR4760 ABB6675	ABB5872. ABB7114. ABP6956. ABG4833. ABB2831.	ABB1895 AAM5427 AAM6666 AAM1453 AAM2695 ABM0225	AAB4249 ABP75877 ABB59056 ABB9733 ABB6316 ABB7093
8488888	22222	22442		2222222	444444
126 126 88 86 86 86	3111 2951 5533	5560 1931 3664 1333	1430 1833 895 2665 2665	22 22 22 22 22 22 22 22 23 23 23 23 23 2	3266 3021 2296 1554 117 1501
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24444	21811	12 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5	336876	8 4 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8	86 4 4 4 4 4 8 6 4 4 4 4 4 8

ALIGNMENTS

AAB73488 standard; Protein; 1590 AA. AAB73488; RESULT 1

25-JUL-2001 (first entry)

Mouse Rim2, a novel isoform of Rim.

pancreatic beta-cell; diabetes; parotid gland; zinc finger; PDZ domain; C2 domain. fouse, murine, Rim2, Rim isoform, Rab3-interacting molecule, intracellular vesicle fusion regulator exocytosis; hormone secretion; neurotransmitter exchange factor; CAMP-GEFII; GDP/GTP

Mus musculus

RP1090986-A1

11-APR-2001.

31-JUL-2000; 2000EP-0116148.

08-OCT-1999; 99JP-0288372.

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(JCRP-) JCR PHARM CO LTD. (SEIN/) SEINO S.

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New Rim 2 proteins and nucleic acids encoding the protein useful in diagnosing endocrine-related diseases or neuropathy and in developing agents for the prevention or treatment of such diseases

Claim 1; Page 10-19; 42pp; English.

This sequence represents mouse Rim2. Rim2 is a novel isoform of Rim (Rab3-interacting molecule, also referred to in the specification as Rim1), and both proteins contain a zinc finger, DZ and two CZ domains. Rim2 is able to specifically interact with the GTF/GDP exchange factor CAMP-GERII, a CAMP sensor molecule, and the GTF/GDP exchange factor CAMP-GERII, a CAMP sensor molecule, and is believed to be a regulator of Rab3-dependent intracellular vesicle fusion in neurons and endocrine tissue. It is therefore likely to play a key role in neurotransmitter release at presynaptic membranes, and in hormonal secretion. The Rim2 procein is useful in diagnosing, and in hormonal secretion. The Rim2 procein is useful in diagnosing the prevention or treatment of such diseases. Rim2-specific hybridisation probes or antibodies are useful in the diagnosis of brain of central nervous system disorders, or for diagnosis of secretion disorders of the prevention and parotid gland, hypothalamus, pancreatic beta-cells and parotid gland.

1590 AA; Sequence

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OQQBQKGDAPTCGICHKTKPADGCGHNCSYCQTKPCARCGGRVSLRSNKVMMVCNLCRKQ 180 240 480 IPLDRPDMRRADSLRKQHHLDPSSAVRKTKREKMETMLRNDSLSSDQSESVRPPPRRPHK 540 KERHKAQPTQWPPPSGITELVNNVLQPQOKQPNEKEPQTKLHQQFEMYKEQVKKKMGEESQ 120 KEEHKAQPIQMPPFSGITELVINVVLQPQQXQPINEKEPQTXCHQQPEMYKRQVKKMGRESQ 120 PSDGIMPRSPSDYADRRSQREPQFYBEPGHLAYRDSNRRGHRHSKEYIVDDEDVBSRDEY 360 SKKGGKMRQVSLSSSEEELASTPRYTSCDDVELESESVSEKGDSQKGKRKTSEQGVLSDS 600 PSDGTMPRSPSDYADRRSQREPQFYEEPGHLNYRDSNRRGHRHSKEYIVDDEDVBSRDEY 360 BRORREKRYQARYRSDPNLARYPVKPOPYEROMRIHAEVSRARHERRHSDVSLANARLED 420 9 QEILTKSGAWFYNSGSNTLQQPDQKVPRGLRNBRAPQBKKAKLHBQPQPQGAPGDLSVPA SKKGGKMRQVSLSSSBEBLASTPRYTSCDDVELESESVSEKGDSQKGKRKTSRQGVLSDS 1 MSAPLGPRGRPAPTPAASQPPPQPEMPDLSHLTEERKIILAVMDRQKKEBERGGSVLKI VEKGRAHGLTRODTIKNGSGVKHQIASDMPSDRKRSPSVSRDQNRRYBQSBERBDYSQYV SRISLLRWDRPSRORSVSERRAAMENORSYSMERTREAOGOSSYPORTSNHSPPTPRRSP 1 MSAPLGPRGRPAPTPAASQPPPQPEMPDLSHLTEEERKIILAVMDRQKKEEEKEQSVLKI Gaps DB 22; Length 1590; ö 0; Indels 100.0%; Score 8285; 100.0%; Pred. No. 0; tive 0; Mismatches Best Local Similarity 100. Matches 1590; Conservative 61 421 481 61 121 181 181 241 241 301 301 361 361 421 481 Query Match 121 음 중 음

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1080 1020 1020 1080 1380 1200 1260 1320 1320 1440 1380 1440 1500 1500 1560 960 780 9 720 720 780 840 840 900 900 LPSREDCRPRAPYVCI YFLPDRSDKNRRRTKTVKKTLBPKNNQTFI YSPVHRREFRERG. 961 LHGESPTRALGRSKRISDSEVSDYDCEDGYGVYSDYRHNGRDLGSSTLSYPEGYWSSNHC DGDR.L.GRILLLANKRLKDGSVPRDSGAM.GLKVVGGROTIBSGRLCAFTTKVKKGSLADTVG HIRPODKYLSWAGRLLQGATFEEVYNILLESRPEPQVELVVSRPIGDIPRIPDSTHAQLE 88888FRSQRMDRPSISVISFMSPGMLRDVPQFLSGQLGIRLMFDKWGHQLLVTILGARD SPSGSPHRVDVIGRTESWSPSAPPPQRNVBQTRGTRATGHYNTISRNDRHRVMDDHYSS 1021 SPSGSPHRVDVIGRTRSWSPSAPPPQRNVBQGHRGTRATGHYNTISRNDRHRVMDDHYSS 1141 ALSRSHPRIGSVQTSPSSTPGTGRRGRQLPQLPPKGTLERGAMDIEERRAMRQMRCLNKYKQV AGSDFRIRQDYHSKTRSGWDFHRGADTVSTRSSDSDVSDVSAVSRIGSBGRFGSTSYMSV OSERPRGNRISVPTSKWONRÇMGVSGRULIKSTSISGDWCSLERNDGSQSDIAVGALGT SGKKRRSSIGAROVALVGLSRKSRSASQLSQTBGGGKKLRSTVQRSTBTGLAVEARUMMT RQASRESTDGSMNSYSSEGNLIFFGVRLASDSQFSDFLDGLGPAQLVGRQTLATPAMGDI DGDRLIGRILLINKRLXDGSVPRDSGAMLGLKVVGGRMTBSGRLCAFITKVKKGSLADTVG HLRPGDBVLEMNGRLLQGATFREVYNI I LESKPBPQVELVVSRPIGDI PRI PDSTHAQLE SSSSSFESQXMDRPSISVTSPMSPGMLRDVPQFLSGQLSIXLMPDXVGHQLIVTILGAXD LPSREDGR PRINPYVKI YPLPDRSDKIKRRTKTTKTLBPKNIOTPI YSPVHRREPRERML 901 BITLMDGARVREESSBFLGBILIKLKTALLDDRPHMYKLQTHDV8SLPLPRPSPYLPRRQ 1141 ALSRSHPRIGSVQTSPSSTPGTGRRGRQLPQLPPKGTLERSAMDIERRNRQMKLNKYKQV AGSDPRI.EQDYHSKYRSGWDPHRGADTVSTKSSDSDVBDVSAVSRTSBASRPSSTSYMSV QSERPRGNRKI SVFTSKMQNRQMGVSGKNLTKSTSI SGDMCSLEKNDGSQSDTAVGALGT SGKKRRSSIGAKNVAI VGLSRKBRSASQLSQTBGGGKKLRSTVQRSTRTGLAVEMRNWYT 1381 RQASRESTDGSMNSYSSBGNLIFPGVRLASDSQFSDFLDGLGPAQLVGRQTLATPAMGDI 1590 SLVDPTSAPLTRRASQSSLESSTGPSYSRS 841 901 1201 199 199 721 721 781 781 841 1021 1081 1081 1201 1261 1261 1321 1321 1381 1501 1501 1561 8 6 8 6 욢 ò 8 8 名 ద 셞 뭐 셤 ठ 8 ò B Š Š ద ò ð 윰 à δ 윱 ð 셤 ò 셤 8 셤 à 셤

ABP63531 standard; Protein; 427 ABP63531 ID ABP(XX RESULT

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Matches
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                                                                                                                                                                                                                                                          Molecular interaction, haematopoletic cell; immune response; T cell; PDZ domain; B cell; endothelial cell; PDZ protein; PSDPS; PDZ ligand; Drosophila large disc protein; Zonula Occludin 1 protein; PL protein; immunosuppressive, antificialmatory; antiallergic; antiatherosoclerotic; antinicrobial; westropic; inflammatory immune response; inflammatory immune response; inflammatory immune response; inflammatory immune response; inflammatory immune response; inflammatory immune response; autoing a linflammatory bowel disease; iletis; enteritis; psoriasis; scleroderma; inflammatory dermatosis; respiratory allergic disease; asthma; cancer; allergic rhinitis; transplantation rejection; atherosclerosis; ischaemia; anglogenesis-dependent disorder; infectious disease.
                                                                                                                                                                                KIAA 0751 PDZ domain related amino acid sequence #1.
                                                                                        28-OCT-2002 (first entry)
         ABP63531;
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Homo sapiens. Synthetic.

WO200242422-A2

30-MAY-2002

09-NOV-2001; 2001WO-US44138.

11-NOV-2000; 2000US-0710059.

24-NOV-2000; 2000US-0721915. 24-NOV-2000; 2000US-0722069. 28-NOV-2000; 2000US-0724553.

(ARBO-) ARBOR VITA CORP.

Lu P, Rabinowitz JD, Schweizer J;

WPI; 2002-608221/65.

Modulating the biological function of an endothelial cell or hematopoletic cell e.g., a T-cell or B-cell comprises introducing into the cell, an agent that inhibits binding of a PDZ protein and a PDZ ligand protein in the cell -

Example 3; Page 165; 207pp; English.

function of an endothelial cell or haematopoietic cell. Mi comprises
introducing into the cell, an agent that inhibits binding of a PDZ
(FBSD95, Drosophila large disc protein, and zonnia occludin 1 protein)
protein and a PDZ ligand (PL) protein in the cell, and so modulates the
biological function. Also described is a method (M2) for determining
whether a test compound is an inhibitor of binding between a PDZ protein
and a PL protein. Mi is used for modulating a biological function of an
endothelial cell or haematopoietic cell e.g., T-cell or B-cell, by an
inflammatory or humoral immune response, or an autoimmune disease. An
inhibitor (I) is useful for treating a disease characterised by leukocyte
activation, where the disease is characterised by an inflammatory or
humoral immune response, e.g., an autoimmune disease. The compounds
e.g., PL-PDZ interaction inhibitors are useful for treating (ameliorating
symptoms of) a variety of diseases and conditions characterised by
inflammatory bowel diseases ulcerative colitis, inflammatory and humoral immune responses e.g., inflammatory and memoral immune responses e.g., inflammatory well alleragic chinitis, ileitis and enteritis,
c psoriasis and inflammatory dermatoses e.g., inflammatory and humoral immune responses e.g., inflammatory powel diseases and conditions characterised by
c inflammatory bowel diseases ulcerative colitis, independent diseases, cadaver,
autologous, bone marrow, xenotransplantation, atherosclerosis, cadaver,
autologous, bone marrow, xenotransplantation, atherosclerosis, cancers,
autologous, bone marrow, xenotransplantation, atherosclerosis, cadaver,
autologous, bone marrow, xenotransplantation, atherosclerosis,
c ABB96620 to AB996732 and ABP63153 to ABP65578 represent sequences used The present invention describes a method (M1) for modulating a biological in the exemplification of the present invention.

26.7%; Score 2215; DB 23; Length 427;

427 AA;

Query Match

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971 QRSKRISDSEVSDYDCEDGVGVVSDYRHMGRDLQSSTLSVPRQVMSSNHCSPSGSPHRVD 1030
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                                                                                                                                                                                                                                                                                                                               242 NPYVKLYPLPDRSDKNKRRTKTVKKTLEPKWNQTFIYSPVHRREFRERMLBITLMDQARV 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                             362 QRSKRISDSEVSDYDCDDGIGVVSDYRHDGRDLQSSTLSVPRQVMSSNHCSPSGSPHRVD 421
                                                                                                                                                                                                   122 WNGKLLQGATFEEVYNIILESKPEPQVELVVSRPIGDIPRIPDSTHAOLESSSSSFESOK 181
                                                                                                                                                                                                                                                               182 MORPSISVTSPWSPGMLKDVPQFLSGQLSIKLWFDKVGHQLIVTILGAKDLPSREDGRPR 241
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                                                                                                                                 62 LINKRLKDGSVPRDSGAMLGLKVVGGRATESGRLCAFITIKVKKGSLADTVGHLRPGDBVLE 121
                                                                                                                                                                                                                                            791 MDRPSISVTSPMSPGMLRDVPQFLSGQLSIKLWPDKVGHQLIVTILGAKDLPSREDGRPR 850
                                                                               13
                                               611 MYYGGHSLERDLEWSRPQIKDSGVDTCSSTTLNERHSHSDKHPVTWQPSKDGDRLIGRIL
                                                                     2 MYPQGASLEEDLEWSEPQIKOSGVDTCSSTTLMERHSHSDKHPVTMQPSKDGDRLIGRILL
                                                                                                                                                                             731 WNGRLLQGATFEEVYNIILESKFEFQVELVVSRPIGDIPRIPDSTHAQLESSSSFESQK
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centered around amino acid 350"
                 Indels
98.6%; Pred. No. 6.2e-147; iive 5; Mismatches 1;
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269
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372
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAW29640 standard; Protein; 374 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Secreted protein; CO618_1; human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human secreted protein CO618_1.
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97US-0072103.
97US-0877035.
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                 419; Conservative
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 Local Similarity
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Claim 22; Page 71-72; 104pp; English. (GEMY) GENETICS INST INC Agostino MJ, Jacobs K, Racie LA, Spaulding V, WPI; 1998-414101/35 N-PSDB; AAV40485

374 AA; Sequence

WMTRQASRESTDGSMNSYSSEGNLIFPGVRLASDSQFSDFLDGLGPAQLVGRQTLATPAM 1437 LGTSGKKRRSSIGAKMVAIVGLSRKSRSASQLSQTEGGKKLRSTVQRSTETGLAVEMRN 1377 61 LGTSGKKRRSSLGAKWAIVGLSRKSRSASQLSQTSAGGKKLRSTVQRSTBTGLAVENKN 120 1 MSVQSERPGGNKKISVFTSKNQSRQMGISGKNMTKSTSISGDMCSLEKNDGSQSDTAVGT 60 1258 MSVQSERPRGNRKISVFTSKMQNRQMGVSGKNLTKSTS1SGDMCSLEKNDGSQSDTAVGA 41; Gaps 1438 GDIQVGMMDKKGQLEVBIIRARGLVVKPGSKTLPAPYVKVYLLDNGVC-Matches 321; Conservative Query Match Best Local Similarity 1378 1318 셤 셤 용 ⋧ δ ð Š

301 LQIIVWGDYGRWDHKSFWGVAQILLDELELSNWYIGWFKLPPPSSLVDPTLAPLTRRASQ 360

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AAB34848 standard; Protein; 237 AA. AAB34848

26-JAN-2001 (first entry)

Lavallie ER, McCoy JM, Merberg D;

Treacy Mi

Human secreted protein sequence encoded by gene 46 SEQ ID NO:136.

Human, secreted protein; diagnosis; cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral; antiallergic; hepatotropic; antidiabetic; antifilammatory; antiulcer; vulnerary; antiformulasut; antibacterial; antifungal; antiparasitic; cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder; wound healing; neurological disease; infectious disease; chromosome identification; chromosome 6.

Homo sapiens.

MO200058356-A1

05-0CT-2000

22-MAR-2000; 2000WO-US07535.

99US-0126511 26-MAR-1999;

99U8-0172413. (HUMA-) HUMAN GENOME SCI INC 17-DEC-1999;

Rosen CA, Ruben SM, Komatsoulis G;

WPI; 2000-594639/56.

Fifty nucleic acid molecules encoding human secreted proteins, useful in the prevention, treatment and diagnosis of cancer, immune disorders, cardiovascular disorders and neurological diseases -

Disclosure, Page 419-420; 425pp; English

The polymucleotide sequences given in AAC59966 to AAC60015 encode the human secreted proteins given in AAB34773 to AAB34822. AAB34823 to human secreted proteins given in the sequences and proteins to consider the proteins in the exemplification of the present invention. Human secreted proteins have activities based on the tissues and cells the genes are expressed in. Examples of activities include: cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral; antiallargic; hepatotropic; antidabetic; antifungal, antiparasitic; and cardiant. The polymucleotides and polympetides are useful for cardiant. The polymucleotides and polympetides are useful for preventing, treating or amelorating a medical condition in e.g. humans, once, rabbits, goats, horses, cats, dogs, chickens or Bheep. The polymucleotides are also be used as a food additive or preservative to increase or decrease storage capabilities. The polymucleotides are useful for chromosome identification. They are also useful as probes for diagnosing a disorder related to the female reproductive system, particularly breast and ovary ancer. They are also useful in the gene therapy of breast and ovary and cancer. Nucleic acids, protein, antibodies, candiovascular disorders, wound healing, neurological diseases and continued the account it finetions disease, and the present invention are useful in the continued and prevention of cancer immune disorders. used in the exemplification of the present invention.

237 AA; Sequence

Ä 1, Gaps Query Match 12.3%; Score 1015.5; DB 21; Length 237; Best Local Similarity 82.8%; Pred. No. 4.6e-63; Matches 197; Conservative 19; Mismatches 21; Indels 1;

ક 셤 OFSDFLDGLGPAQLVGRQTLATPAMGDIQVGMMDKKGQLRVRIIRARGLVVKPGSKTLPA 1472 OFSDFLDGLGPAQLVGRQTLATPAMGDIQIGMEDKKGQLEVEVIRARSLTQKPGSKSTPA 119 1413

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New isolated polynucleotides and secreted proteins - obtained from human foetal kidney, adult testes, placenta, adult brain and foetal brain cDNA libraries

This is the amino acid sequence of novel human secreted protefn CO618 1, as predicted from human adult brain cDNA clone CO618 1 (see AN40465). CO618 1 cDNA was isolated using methods which are selective for cDNAs encoding secreted proteins, and was identified as encoding a secreted or transmembrane protein on the basis of as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. CO618 1 shows some sequence similarity to rat Rim, a protein. CO618 1 shows some sequence similarity to rat Rim, a protein and foetal human foetal proteins (see AAW29636-45) adult brain and foetal brain, and can be obtained by expression in recombinant host cells. The polypeptides may have e.g. mutritional crivity, immunostimulant or immunosuppressive activity, haematopoiesis regulating activity, tissue growth activity, activity, chocking and cell proliferation or differentiation activity, haematopoiesis regulating activity, rissue growth activity, haematopoiesis regulating activity, receptor/ligand activity, antifinammatory activity, canherin or tumour invasion suppressor activity, tumour inhibition activity, or other activities.

19.1%; Score 1586.5; DB 19; Length 374; 85.8%; Pred. No. 7.1e-103; ive 6; Mismatches 6; Indels 41;

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1517 LQIIVMGDYGRMDHKSFMGVAQILLDELELSNMVIGWFKLFPPSSLVDPTSAPLTRRASQ 1576

AAB34848

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The polynuclectide sequences given in AAG59966 to AAG60015 encode the human secreted proteins given in AAB34773 to AAB34822. AAB34823 to AAB34822 represent human secreted polypeptide sequences and proteins to man secreted proteins have activities based on the tissues can decila the genes are expressed in Examples of activities in the present invention. Human secreted proteins have activities based on the tissues and cells the genes are expressed in Examples of activities include: cytostatic; immunosuppressive, nootropic; neuroprotective; antividate include: cytostatic; immunosuppressive, nootropic; neuroprotective; antividate cytostatic; immunosuppressive, nootropic; neuroprotective; antividate cytostatic; anticonvulsant; antibacterial; antifungal; antiparasitic; and cardiant. The polynucleotides are useful for cytostating, treating or ameliorating a medical condition in e.g. humans, mice, rabbits, goats, horses, cats, dogs, chickens or sheep. The polynucleotides are useful for chromosome identification. They are also useful as probes for diagnosing a disorder related to the female reproductive system, carciant and ovarian cancer. They are also useful in the gene therapy of breast and ovarian cancer. Nucleic acids, protein, antibodies, agonists and antagonists from the present invention are useful in the cardiovascular disorders, wound healing, neurological diseases and in the exemplification of the present invention.
PYVKVYLLDNGVCIAKKKTKVARKTLBPLYQQLLSFBESPQGRVLQIIVMGDYGRNDHKS 1532
                   120 PYVKVILLENGACIAKKKTRIARKTLDPLYQQSLVPDSSPQGKVLQVIVWGDYGRMDHKC 179
                                                                               PMGVAQILLDBLELSNMVIGWFKLPPPSSLVDPTSAPLTRRASQSSLBSSTGPSYSRS 1590
                                                                                                                                                                                                                                                                                                                                                                                                                            nootropic; neuroprotective; antiviral; antiallergic; hepatotropic; antidabetic; antinilammatory; antiulcer; vulnerary; anticonvulsant; antibacterial; antifungal; antiparastic; cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder; wound healing; neurological disease; infectious disease; chromosome identification.
                                                                                                          FWGVAQILLEELDLSSMVIGWYRLFPPSSLVDPTLTPLTRRASQSSLESSTGPPCIRE 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fifty nucleic acid molecules encoding human secreted proteins, useful in the prevention, treatment and diagnosis of cancer, immune disorders, cardiovascular disorders and neurological diseases
                                                                                                                                                                                                                                                                                                                                                                Gene 46 human secreted protein homologous amino acid sequence #135.
                                                                                                                                                                                                                                                                                                                                                                                                          Human; secreted protein; diagnosis; cytostatic; immunosuppressive;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rosen CA, Ruben SM, Komatsoulis G;
                                                                                                                                                                                                                                    AAB34847 standard; Protein; 237 AA
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                                                                                                                                                                                                                                                                                                                        (first entry)
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PYNYVILDNGVCIAKKKTKVARKTLBPLYQQLISFBRBPQGRVLQIIVMGDYGRMDHKS 1532
                                                                                                                                                                                                    1353 EGGGKKLRSTVQRSTETGLAVEMRNWMTRQASRRSTDGSMRSYSSEGMLIPPGVRLASDS 1412
                                                                                                                                                                                                                                                                                                                                         QPSDFLDGLGPAQLVGRQTLATPAMGDIQVGMMDKKGQLKVRIIRARGLVVKPGSKTLPA 1472
                                                                                                                                                                                                                                                                                                                                                                                   60 QPSDFLDGLGPAQLVGRQTLATPAMGDIGNGADKKGQLEVEVIRARSLTQKPGSKSTPA 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 120 PYVKYYLLENGACIAKKGTRIAKKTLDPLYQQSLVFDSSPQGKVLQYIVMGDYGRMDHKC 179
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PMGVAQILLDELELSNMVIGWFKLPPPSSLVDPTSAPLTRRASOSSLESSTGPSYSRS 1590
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  180 FWGVAQILLEELDLSSMVIGWYKLFPPSSLVDFTLAPLTRRASGSSLEBSSGPPCIRS 237
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL16111), expressed DNA sequences (ABL16176-ABL16111), expressed DNA
                                                                                                                                                                                                                                              1 BSGHICKLKSTIQRSTETGWAARWEK-MYRQDSRBSTDGBINSYSSEGWLIPPGVRVGPDS
                                                                                                                                        1; Gaps
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                                                                         DB 21; Length 237;
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                                                                  Query Match 12.2%; Score 1010.5; DB 21; Length : Best Local Similarity 82.4%; Pred. No. 1e-62; Matches 196; Conservative 20; Mismatches 21; Indels
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11-JUL-2000; 2000US-0614150.
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237 AA;
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QY QRSKRISDSBVSDYDCEDGVGVVSDYKHNGRDLQSSTLSVPEQVMSSNHC 1020	1053	QY 1094	Db 1489 HPQHQPMGYGEPPSSDPAMCGECVDQHFLGGLTGPQLNLGVVPTYHVHTPTPNAHRRARG 1548	1729 SLDLQRTSQQKLYGPAAPYLKRRRILPHPPSAQNAHNFSPMEPGSGMDGLKAAAAGAVEQ 1227TVSTKSSDSDVSDVSAVSRTSS
Cuery Match Query Match Best Local Similarity 19.8; Score 989; DB 22; Length 2464; Best Local Similarity 19.88; Pred. No. 1.16-59; Matches 503; Conservative 201; Mismatches 507; Indels 1330; Gaps 73; Qy 272 DRKRSPSYRDQ-NRKYRGSEREDYSQYVEDGTMPKSPSDYADRRSQREPERED 330 Db 20 DLKKPPSKTSQSPLNHPQKNPERQTPSSVYSHTQSTSTTPTGGRLQVRTSLDPWRQCRS 77 QY 331 LANYRDSNRRG	Db 78 IMERDILISSGAGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	541 SKKGGKURQVSIGSSERELASTPEYTSCDDVELESESVSEKGDSQKGRKKTSIGSSERELASTPEYTSCDDVELESESVSEKGDSQKGRKKT	Oy 681 PRDSGAMLGLKVVGGK	0.5 0.5

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-------DMCSLEKNDGSQ8-----DTAVGALGTS 1321
                   2029 ADADADAPLDAIDWDAIDAMLDDDRSBYDKDKDABBAGGSKSARGAGABAKVDGSLSDI 2088
                                                                                                 1370 -----GLAVERINET-- 1380
                                                                                                               2143 TGGGLGVSLGGAGGAAGGSGAGGGLSRGSSSEVDAIEQFFGDGAGGESLKLDTWVQLR 2202
                                                                                                                                                                         2203 LFVVSRQRQYQAQFAIAGSSTSSAGHHHITLPPPHPYHQRQSRGSAGSIQRSVBVPPVPP 2262
                                                                                                                                                                                                 ----TDGSMNSY-SSEGNLIFPGVRLASDSQPSDFLDGLGPAQLVGRQTLATPAMGDIQV 1442
                                                                                                                                                                                                              GMMDKKGQLKVBIIRARGLVVKPGSKTLPAPYVKYYLLDNGVCIAKKKTKVARKTLEPLY 1502
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AAB34849 standard; Protein; 134 AA. RESULT 7

AAB34849;

(first entry) 26-JAN-2001

Gene 46 human secreted protein homologous amino acid sequence #137.

Human; secreted protein; diagnosis; cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral; antiallergic; hepatotropic; antidabetic; antiinflammatory; antiulcer; vulnerary; antionvulsant; antibacterial; antifungal; antiparasitic; cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder; wound healing; neurological disease; infectious disease; chromosome identification. Human; secreted protein; diagnosis;

Rattus norvegicus.

WO200058356-A1

05-OCT-2000,

22-MAR-2000; 2000WO-US07535.

99US-0126511. 26-MAR-1999; 17-DEC-1999;

(HUMA-) HUMAN GENOME SCI INC

Komatsoulis G; Ruben SM, Rosen CA,

#PI; 2000-594639/56.

Fifty nucleic acid molecules encoding human secreted proteins, useful in the prevention, treatment and diagnosis of cancer, immune disorders, cardiovascular disorders and neurological diseases -

Disclosure; Page 420-421; 425pp; English.

The polymuclectide sequences given in AACS9966 to AAC60015 encode the human secreted proteins given in AAB34773 to AAB34822. AAB34823 to AAB34822 represent human secreted polymeptide sequences and proteins in homologous to them, which are given in the exemplification of the present invention. Human secreted proteins have activities based on the tissues of and cells the genes are expressed in. Examples of activities include: Crostatic, immunosuppressive, nootropic; neuroprotective; antivital; anticornulsant; antibacterial; antifungal; anticornulsant; antibacterial; antifungal; antivites; cardiant. The polymucleotides and polymeptides are useful for cardiant. The polymucleotides and polymeptides can also used needs a food additive or preservative to increase or decrease storage capabilities. The polymucleotides are useful for chromosome identification. They are also useful as probes for increase or decrease storage capabilities. The polymucleotides are useful for chromosome identification. They are also useful in the gene therapy of breast and/or ovary cancer. They are also useful in the gene therapy of breast and/or ovary cancer. They are also useful in the capanists and antagonists from the present invention are useful in the disonders, treatment and prevention of cancer, immune disorders, calling the present invention are useful.

Cardiovascular disorders, wound healing, neurological diseases and infectious diseases. AACS9955 and AACS99 used in the exemplification of the present invention. 88888888888888888888888888

134 AA; Sequence

0; Gaps Query Match 7.5%; Score 624; DB 21; Length 134; Best Local Similarity 85.1%; Pred. No. 6.1e-36; Matches 114; Conservative 11; Mismatches 9; Indels (

884 944 9 825 DKVGHQLIVTIIGAKDIPSREDGRPRNPYVKIYFLPDRSDKNKRRTKTVKKTLBPKNNQT 885 FIYSPVHRREFRERMLEITLWDQARVREEBSEFLGBILIELETALLDDEPHWYKLQTHDV н ò 줨 ò B

945 SSLPLPRPSPYLPR 958

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ABB15089 standard; Protein; 158 AA.

ABB15089;

(first entry) 23-JAN-2002

Ruman nervous system related polypeptide SEQ ID NO 3746.

Human; nootropic; neuroprotective; cytostatic; dermatological; virucide; immunosuppressive; antiinflammatory; anti-HIV; antibacterial; vulnerary; antiparinsonian; antialckling; antianaemic; antiarthritic; cancer; antitheumatic; hepatotropic; cerebroprotective; antiinflammatory; antiallergic; antidiabetic; antiunicer; anticonvulaent; antifungal; antiparasitic; cardiant; immune disorder; cardiovascular disorder; neurological disease; infection; nephrotropic; gene therapy; vaccine.

Homo sapiens.

WO200159063-A2

16-AUG-2001.

17-JAN-2001; 2001WO-US01334

31-JAN-2000; 2000US-0179065. 04-FEB-2000; 2000US-0180628. 24-FEB-2000; 2000US-0184664. 02-MAR-2000; 2000US-0186350.

(HUMA-) HUMAN GENOME SCI INC. Ruben Rosen CA, Barash SC, WPI; 2001-541565/60. N-PSDB; ABA11415.

Nucleic acids encoding 3224 human nervous system antigen polypeptides, useful for preventing, diagnosing and/or treating nervous system cancers and metastases -

Claim 11; SEQ ID NO 3746; 1701pp + Sequence Listing; English

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The invention relates to novel genes (ABA11004-ABA21534) and proteins (ABB14678-ABB18001) useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (ant) agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune disorders e.g. Addison's disease, allergies, autoimmune charmolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c) cardiovascular disorders such as myocardial ischaemias; (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and parasitic infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
6.9%; Score 569.5; DB 22; Length 158;
Best Local Similarity 41.2%; Pred. No. 5.3e-32;
Matches 133; Conservative 3; Mismatches 12; Indels 175; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               158 AA;
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(HUMA-) HUMAN GENOME SCI INC

99US-0126511. 99US-0172413.

26-MAR-1999; 17-DEC-1999;

22-MAR-2000; 2000WO-US07535.

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1068 MDRHRVMDDHYSSDRDRDCEAADRQPYHRSRSTEQRPLLERTTTRSRSSERPDTNLMRSM 1127
                                                                        1128 PSIATGRSAPPSPALSRSHPRTGSVQTSPSSTPGTGRRGRQLPQLPPKGTLKRSAMDIEK 1187
                                                                                                                                            1188 RNROWKINKYKOVAGSDPRIEQDYHSKYRSGWDPHRGADIVSIKSSDSDVSDVSAVSRIS 1247
                                                                                                                                                                                                                   1248 SASRPSSTSYMSVQSERPRGNRKISVFTSKMQNRQMGVSGKNLTKSTSISGDMCSLEKND 1307
                                                                                                                                                                                                                                                                                             1308 GSQSDTAVGALGTSGKKRRSSIGAKMVAIVGLSRKSRSASQLSQTEGGGKKURSTVQRST 1367
                                                                                         1 MDRHRVMDDHYSPDRDRDCEAADRQPYHRSRSTBQRPLLERTITRSRSTBRPDTXLMRSM 60
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AAB34850 standard; Protein; 128 AA (first entry) 26-JAN-2001 AAB34850;

Human secreted protein sequence encoded by gene 46 SBQ ID NO:138.

Human; secreted protein; diagnosis; cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral; antiallergic; hepatotropic; antidiabetic; antiinflammatory; antiulcer; vulnerary; anticonvulsant; antidabeterial; antifungal; antiparasitic; cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder; wound healing; neurological disease; infectious disease; chromosome identification; chromosome 6.

Homo sapiens

WO200058356-A1

05-OCT-2000

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The polymuclectide sequences given in AAC59966 to AAC60015 encode the human secreted proteins given in AAB34773 to AAB34822. AAB34823 to human secreted proteins given in AAB34773 to AAB34822. AAB34823 to AAB34822 represent human secreted polymeride sequences and proteins howologous to them, which are given in the exemplification of the present invention. Ruman secreted proteins have activities based on the tissues condected in manneous presents and cells the genes are expressed in. Examples of activities include: cytostatic; immunosuppressive; noctropic; antidabetic; antidalersy; anticonvulsant; antibacterial; antifungal; antiparasitic; and artialersy; anticonvulsant; antibacterial; antifungal; antiparasitic; and cardiant. The polymucleotides are useful for cardiant. The polymucleotides are useful for preventing, treating or ameliorating a medical condition in e.g. humans, condicesse or decrease storage capabilities. The polymucleotides are useful for chromosome identification. They are also useful in the gene conformation and second conformation are useful in the gene conformation and prevention of cancer. Immune disorders, and ovary and cancer. Manued diseases and cancers wound healing, neurological diseases and cancers and in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1446 DKKGQLEVEIIRARGLVVKPGSKTLPAPYVKVYLLDNGVCIAKKKTKVARKTLEPLYQQL 1505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1506 LSFRESPOGRVLQIIVWGDYGRNDHKSFMGVAQILLDELELSNMVIGWFKLFPPSSLVDP 1565
                                                                                                                                                                                                                                                  Fifty nucleic acid molecules encoding human secreted proteins, useful in the prevention, treatment and diagnosis of cancer, immune disorders cardiovascular disorders and neurological diseases -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 DKKGQLEVEVIRARSLTQRPGSKSTPAPYVKVYLLENGACIAKKKTRIARKTLDPLYQQS
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PDZ domain; B cell; endothelial cell; PDZ protein; PSD95; PDZ ligand;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KIAA 0751 PDZ domain related amino acid sequence #2.
                                                                                                                                                                                                                                                                                                                                        Disclosure; Page 421; 425pp; English.
                                                                                                                                                                     Komatsoulis G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABP63532 standard, Protein, 92 AA.
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                                                                                                                                                                                                               WPI; 2000-594639/56.
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120

Drosophila large disc protein; Zonula Occludin 1 protein; PL protein; immunosuppressive; antinflammatory; antiallergic; antiatherosclerotic; antiulcer; antiporiatic; dermatological; antianfmatic; cytostatic; antimicrobial; vasotropic; inflammatory immune response; inflammation; humoral immune response; autoimmune disease; allergy; ulcerative colitis; humoral immune response; iletitis; enteritis; psoriasis; scleroderma; inflammatory dermatosis; respiratory allergic disease; asthma; cancer; allergic rhinitis; transplantation rejection; atherosclerosis; ischaemia; angiogenesis-dependent disorder; infectious disease.

Homo sapiens. Synthetic.

WO200242422-A2.

30-MAY-2002

09-NOV-2001; 2001WO-US44138.

11-NOV-2000; 2000US-0710059,

24-NOV-2000; 2000US-0721915. 24-NOV-2000; 2000US-0722069. 28-NOV-2000; 2000US-0724553.

(ARBO-) ARBOR VITA CORP.

Schweizer J; Lu P, Rabinowitz JD,

WPI; 2002-608221/65.

Modulating the biological function of an endothelial cell or hematopoietic cell e.g., a T-cell or B-cell comprises introducing into the cell, an agent that inhibits binding of a PDZ protein and a PDZ ligand protein in the cell

Example 3; Page 165; 207pp; English.

The present invention describes a method (M1) for modulating a biological function of an endothelial cell or haematopoietic cell. M1 comprises carrivolucing into the cell, an agent that inhibits binding of a PDZ (PSD95, Drosephila large disc protein, and Zomula occludin 1 protein) protein and a PDZ ligand (PL) protein in the cell, and so modulates the biological function. Also described is a method (M2) for determining whether a test compound is an inhibitor of binding between a PDZ protein and a PL protein. M1 is used for modulating a biological function of an cinclial cell or haematopojotetic cell e.g., T-cell or B-cell, by an inflammatory or humoral immune response, or an autoimmune disease. An inhibitor (I) is useful for treating a disease characterised by leukocyte activation, where the disease is characterised by an inflammatory or humoral immune response, e.g., an autoimmune disease. The compounds c, PDDZ interaction inhibitors are useful for treating (ameliorating symptoms of) a variety of diseases and conditions characterised by inflammatory bowel diseases and conditions characterised by inflammatory bowel diseases, ulcerative colitis, ilettis and enteritis, inflammatory bowel diseases, ulcerative colitis, ilettis and enteritis, cardiac, kidney, lung, liver, small bowel, cornea, pancreas, cadaver, autologous, bone marrow, xenotransplantation, atherosclerosis, cancers, angiogenesis-dependent disorders, infectious diseases and ischaemia.

ABG96620 to ABG96732 and ABB6615318 represent sequences used in the exemplification of the present invention.

92 AA; Sequence

Gaps .. 0 5.6%; Score 464; DB 23; Length 92; 100.0%; Pred. No. 6e-25; 0; Indels 100.0%; Pred. no. 91, Conservative Local Similarity Query Match Matches

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735 LLQGATPEEVYNIILESKPEPQVELVVSRPI 765

61 LLQGATFBEVYNIILESKPBPQVELVVSRPI 91 윰

AAB40725 standard, Protein, 126

AAB40725;

08-FEB-2001 (first entry)

Human ORFX ORF489 polypeptide sequence SEQ ID NO:978.

Human; open reading frame; ORFX; detection; cytostatic; hepatotropic; vulnerary; antipsoriatic; antiparkinsonian; nootropic; neuroprotective; anticorvulsant; osteopathic; antiparthritic; immunosuppressate; cardiant; immunostimulant; thrombolytic; cagulant; vasotropic; antidiabetic; hypotensive; dermatological; immunosuppressive; antidialammatory; hypotensive; antibacterial; antifungal; antianematic; antibacterial; antifungal; antianematic; antidacent; proliferative disorder; hypothyroid; antianaemic; gene therapy; cancer; proliferative disorder; hypothyroid; antianaemic; defendation; osteoarthritis; graft vs host disease; cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS; cholesterol ester storage; systemic lupus erythematosus; infection; severe combined immunodeficiency; malaria; autoimmune disorder; asthma; molendamage; cartilage damage; antiinflammatory disease; coagulation; thrombosis; contraceptive.

Homo sapiens.

MO200058473-A2.

35-OCT-2000.

31-MAR-2000; 2000WO-US08621.

31-MAR-1999; 02-APR-1999;

99US-0127607. 99US-0127636. 99US-0127728. 30-MAR-2000; 2000US-0540763 05-APR-1999;

(CURA-) CURAGEN CORP.

Leach M; Shimkets RA,

WPI; 2000-602362/57. N-PSDB; AAC74934.

Novel nucleic acids and peptides derived from open reading frame X, neurodegenerative disorders and cardiovascular disease cancers, proliferative for treating

Claim 11; Page 956-957; 5507pp; English.

AAC7446 to AAC77606 encode the proteins given in AAB40237 to AAB43397, which represent the human ORFX open reading frames 1 to 3161. The ORFX sequences have activities such as: cytostatic; hepatotropic; vulnerary; antiportatic; antiportatic; antiportatic; antiportatic; antiportatic; antiportatic; antiformulant; cardiant; thrombolytic; coapulant; vasotropic; antidiabetic; hypotensive; dermatological; immunosuppressive; antidiabetic; hypotensive; dermatological; immunosuppressive; antidiabetic; hypotensive; dermatological; immunosuppressive; antidiabetic; hypotensive; dermatological; immunosuppressive; antidiabetic; hypotensive; dermatological; or preventing or treating the presence of or predisposition to, or preventing or treating the presence of or predisposition to, or preventing or treating pathological conditions associated with an ORFX-associated disorder. The nucleic acids can be used to express ORFX proteins in gene therapy vectors. The proteins and nucleic acids may be used to treat cancers, proliferative disorders, neurodegenerative disorders, osteoarthritis, proliferative disorders, neurodegenerative disorders systemic lupus cythematosus, hypothyroidism, cholesterol ester storage, systemic lupus erythematosus, severe combined immunodeficiency (SCID), AlDS, viral, bacterial or fungal infection, malaria, autoimmune disorders, asthma, AAB4 0725
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Modulating the biological function of an endothelial cell or hematopoietic cell e.g., a T-cell or B-cell comprises introducing into the cell, an agent that inhibits binding of a PDZ protein and a PDZ
allergies, aplastic anaemia, burns, wounds, bone and cartilage damage, nocturnal haemoglobinuria, antiinflammatory disease; to enhance coagulation; to inhibit thrombosis; and as a contraceptive.
                                                                                                                                                                     1358 KLRSTVQRSTBTGLAVENRNWMTRQASRESTDGSMNSYSSEGNLIFPGVRLASDSQPSDF
                                                                                                                                                                                          0; Gaps
                                                                                                     ch 5.1%; Score 420; DB 21; Length 126;
l Similarity 65.3%; Pred. No. 1.2e-21;
81; Conservative 19; Mismatches 24; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KIAA 0751 PDZ domain amino acid sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                              ABP63179 standard; Peptide; 82 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11-NOV-2000; 2000US-0710059.
24-NOV-2000; 2000US-0721915.
24-NOV-2000; 2000US-0722069.
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                                                                                                                     Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2002-608221/65.
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                                                                                                     Query Match
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ABP63179
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introducing into the cell, an agent that inhibits binding of a PDZ

(PSD95, Drosophila large disc protein, and Zonula Occludin 1 protein)

protein and a PDZ ligand (PL) protein in the cell, and so modulates the
biological function. Also described is a method (MZ) for determining

whether a test compound is an inhibitor of binding between a PDZ protein

whether a test compound is an inhibitor of binding between a PDZ protein

compared to the protein. Mi su used for modulating a biological function of an

compared to the season of the season of an entoimmune disease. An
inflammatory or humoral immune response, or an entoimmune disease, An
continuation (N) is useful for treating a disease characterised by leukocyte

compared to the disease is characterised by an inflammatory or
compared to the disease is characterised by leukocyte

compared to a variety of diseases and teoimmune disease. The compounds

compared to a variety of diseases and teoimines of the season of the season of the season of the season of the anterior and humoral immune response e.g., inflammatory and humoral immune response e.g., inflammatory bowel diseases, ulcerative colitis, ileitis and enteritis,
compared to a variety of diseases and inflammatory bowel diseases understand the enterior of the season of the present invention.

condition, where the disease is characterised by an inflammatory bowel diseases, ulcerative colitis, ileitis and enteritis,
compared to the present innerson parteres, cancers,
condiso, kidney, lung, liver, small bowel, cornea, pancreas, cadaver,
autologues, bene marrow, xenoricransplantation, atherosociars cancers,
condisonesis-dependent disorders, infectious diseases and ischaemia.

ABQ96620 to ABQ96732 and ABP63153 to ABP631578 represent sequences used
conditions and infections of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   682 RDSGAMLGLKVVGGKMTESGRLCAPITKVKKGSLADTVGHLRPGDKVLENNGRLLQGATF 741
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5.0%; Score 417; DB 23; Length 82;
100.0%; Pred. No. 1e-21;
1ve 0; Mismatches 0; Indels
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99US-0134117.
99US-0134118.
99US-0160860.
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11-APR-2000; 2000US-0196460.
11-APR-2000; 2000US-0196527.
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14-JAN-2000; 2000US-0176195.
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Best Local Similarity 100...
Best Local 82; Conservative
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21-0CT-1999;
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                                                                                                                                                                 The present invention relates to a new method for modulating a biological function of an endothelial cell or hematopoietic cell. The method involves introducing into a cell, an antagonist that inhibits binding between a PDZ protein and a PL protein. The inhibitor is used to treat a disease mediated by hematopoietic cells, e.g. autoimmune disease. It may also be used to prevent transplantation rejection of a solid organ transplant. The method may also be used in the treatment of inflammation, allergy, inflammatory bowel diseases, ulcerative colitis, ileitis, psoriasis asthma, atopic dermatitis, autoimmune diseases (e.g. rheumatoid arthritis, multiple soletosis, osteoarthritis, insulin-dependent diabetes, Hashimoto thyroiditis, osteoarthritis, inflammation, transplantation rejection), atherosclerosis, cancers, infectious diseases, ischemia, vasulitis and Crohn's disease.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0, Gaps
                                                                    hematopoietic cell, useful for treating autoimmune diseases and infectious diseases, by administering an antagonist that inhibits binding between a PDZ protein and a PL protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                   5.0%; Score 417; DB 22; Length 86;
100.0%; Pred. No. 1.1e-21;
                                                     function of an endothelial cell or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
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                                                                                                                                      Disclosure; Page 28-43; 141pp; English.
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99US-0134117.
99US-0134118.
99US-0160860.
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                                                Modulating a biological
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
                 WPI; 2001-080245/09.
                                                                                                                                                                                                                                                                                                                                                                                                                  86 AA;
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The present invention relates to a method for modulating a biological function of an endothelial cell or haematopoietic cell, comprises introducing into a cell an antagonist that inhibits binding between a PDZ domain protein and a PL domain protein to result in inhibition of leukocyte activation. The present sequence is a PDZ domain. PDZ domains of proteins are named after three prototypical proteins. PDZ domains proteins are named after three prototypical protein. PDZ domains proteins are named after three prototypical protein. PDZ domains proteins are named after three prototypical protein. PDZ domains protein are named after three prototypical protein. PDZ domains protein are involved in synapse formation by organising transmembrane neutotransmitter receptors through intracellular interactions. The inhibitors identified by the present invention can be used to treat a disease mediated by haematopoietic cells, e.g. autoimmune diseases inflammation, allering, psoriasis, respiratory allering ciscases (e.g. rheumatoid arthritis, multiple sclerosis, insulin-dependent diabetes, Habhimoto thyroidtis, orstearthritis, atherosclerosis, cancers, infectious disease. The inhibitors can also be used to prevent transplantation rejection of a solid organ transplant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       682 RDSGAMIGLKVVGGKMTESGRLCAPITKVKKGSLAĎTVŒHLRPGDEVLEMNGRLLQGATF 741
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                                                                                                                                                                                           New inhibitors of binding of a PDZ protein and PL protein for inhibiting T cell-mediated response by hematopoletic cells, or for treating diseases characterized by inflammatory and humoral immune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 / Match 5.0%; Score 417; DB 22; Length 86; Local Similarity 100.0%; Pred. No. 1.1e-21; DB 22; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                               responses, e.g. inflammation, cancer
                                                                                                                                                                                                                                                                                                      Disclosure, Page 36; 139pp; English.
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  11-APR-2000; 2000US-0196460.
11-APR-2000; 2000US-0196527.
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WO200069898-A2

23-NOV-2000

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The present invention relates to a method for modulating a biological function of an endothelial cell or haematopoietic cell, comprises introducing into a cell an antagonist that inhibits binding between a PDZ domain protein and a PDZ domain. PDZ domain. PDZ domain. PDZ domain. PDZ domain. PDZ domain. PDZ domain. PDZ domain. PDZ domain. PDZ domain. PDZ domain. PDZ domain. PDZ domain. PDZ domain. PDZ domain. PDZ domain. PDZ domain. PDZ domain. PDZ domain. PDZ domain. PDZ domain. PDZ domain. PDZ domain. PDZ domain. PDZ domain. PDZ domain. PDZ domain. PDZ domain. PDZ domain. PDZ domain. PDZ domain. PDZ domain. PDZ domain. PDZ domain. PDZ domain. PDZ domain. PDZ domain. PDZ domain. PDZ domain. PDZ domain. PDZ domain. PDZ domain. PDZ domain. PDZ domain. PDZ domain. PDZ domain. PDZ domain. PDZ domain. PDZ domain. PDZ domain. PDZ domain. PDZ domain. PDZ domain. PDZ domain. PDZ domain. PDZ domain. PDZ domain. PDZ domain. PDZ domain. PDZ domain. PDZ domain. PDZ domain. PDZ domain. PDZ domain. PDZ domain. PDZ domain. PDZ domain. PDZ domain. PDZ domain. PDZ domain. PDZ domain. PDZ domain. PDZ domain. PDZ domain. PDZ domain. PDZ domain. PDZ domain. PDZ domain. PDZ domain. PDZ domain. PDZ domain. PDZ domain. PDZ domain. PDZ domain. PDZ domain. PDZ domain. PDZ domain. PDZ domain. PDZ domain. PDZ domain. PDZ domain. PDZ domain. PDZ domain. PDZ domain. PDZ domain. PDZ domain. PDZ domain. PDZ domain. PDZ domain. PDZ domain. PDZ domain. PDZ domain. PDZ domain. PDZ domain. PDZ domain. PDZ domain. PDZ domain. PDZ domain. PDZ domain. PDZ domain. PDZ domain. PDZ domain. PDZ domain. PDZ domain. PDZ domain. PDZ domain. PDZ domain. PDZ domain. PDZ domain. PDZ domain. PDZ domain. PDZ domain. PDZ domain. PDZ domain. PDZ domain. PDZ domain. PDZ domain. PDZ domain. PDZ domain. PDZ domain. PDZ domain. PDZ domain. PDZ domain. PDZ domain. PDZ domain. PDZ domain. PDZ domain. PDZ domain. PDZ domain. PDZ domain. PDZ domain. PDZ domain. PDZ domain. PDZ domain. PDZ domain. PDZ domain. PDZ domain. PDZ domain. PDZ domain. PDZ domain. PDZ domain. PDZ
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                                                                                                                                       99US-0134117.
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99US-0160860.
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                                                       12-MAY-2000; 2000WO-US13205.
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14-FEB-2000; 2000US-0182296.
11-APR-2000; 2000US-0196460.
11-APR-2000; 2000US-0196527.
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0; Gaps Query Match 5.0%; Score 417; DB 22; Length 86; Best Local Similarity 100.0%; Pred. No. 1.1e-21; Matches 82; Conservative 0; Mismatches 0; Indels à

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Search completed: December 12, 2003, 07:13:57 Job time : 84 secs

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OM nucleic - nucleic search, using sw model Run on:

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US-09-617-099B-2 4980

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Scoring table: IDENTITY_NUC Gapop 10.0, Gapext 1.0

2888711 seqs, 20454813386 residues Total number of hits satisfying chosen parameters:

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

GenEmbl:* Database :

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	Bulc	Eukaryota;	Metazoa;		Chordata, Cran	Craniata, Ver	tebrata;
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Kiyomo, S., Shibazaki, T. and Ozaki, N.
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841 ITCAGACAGAAACGAAGTCCATCAGTGTCCAGGGATCAAAATCGAAGATACGAGCAAAG 900 	901 TGAAGAAGAGACTACTCACAGTATGTTCCTTCAGATGGTACAATGCCAAGATCTCC 960 	961 TTCGGATTATGCTGATAGACGATCTCAGCGTGAGCCTCAATTTTATGAAGAACCTGGTCA 1020 	1021 TTTAAATTACAGGGATTCTAACAGGAGAGGCCATAGACATTCCAAAGAGTATATTGTGGA 1080 	1081 TGATGAAGATGTGGAGAGAGATGAATATGAAAGACAAAGGAGGAGGGGGAATACCA 1140 	8=8 8=8	1201 AGAACAAATGCGCATCCACGCTGAGGTGTCCAGGGCACACACA	1261 TGTTTCTTTGGCAAACGCTGAACTAGAAGATTCCAGGATTTCTCTGCTAAGANGGATAG 1320 	8=8		1441 TCATAGTCCTCCCACCCCTCGGCGGAGCCCTATACCGCTTGATAGACCAGACATGAGGCG 1500 	8=8 8=8	2 2 2 3 3 3 3 3 3	6 	1681 TTCACTGAGCTGGAGGAGGAGGAGCTTCCACACCTGAGTATACAAGCTGTGATGA 1740 	1741 TGTGGAGCTGGAAAGCGAGAGTGTGAGTGAGGGGGACAGTCAAAAGGGAAAAAGAAA 1800 1741 TGTGGAACTGGAAAAGTGAAGTGAGAAAAGGGACAGTCAAAAGGAAAAAAAA	1801 AACTAGTGAGGGGGGGTTTTTGTCGGATTCTAACACGGGTCTGAGAGGAAAGGAAAG 1860 		

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TLEPLYQDLLSFESPQGRVLGITVWGDSSTLBSTGPSYSRS*

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                                                                                           2 (bases 1 to 4800)
Ozaki, N. and Seino, S.
Direct Submission
Submitted (12-DSC-1998) Nobuaki Ozaki, Nagoya University School
Medicine, First Department of Internal Medicine, Nagoya, Nagoya
466-8550, Japan (R-mail:n-ozaki@med.nagoya-u.ac.jp,
Tel:81-52-74-2142, Fax:81-52-744-2157)
Sequence updated (02-7eb-2000)
Location/Qualifiers
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    CAMP-GEFII is a direct target of CAMP in regulated Nat. Cell Biol. 2 (11), 805-811 (2000)
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Db 2341 AATACCTGATAGCACGCATGCACAACTGGAATCCAGTTCTAGCTCATTTGAATCTCAAAA 2400	OY 2401 AAINGAACCSTCCTTCTATATCCGTTACCTCACCATGAGTCCTCGGCATGCTGAGGGATGT 2460 Db 2401 AAINGAACCSTCCTTCTATATCCGTTACCTCACCCATGAGTCGTGGCTGGC	OY 2461 CCCGCAGTTCTTALCTCGACCTTTCAATAAACTATGGTTTGACGAGGTTGGTCACCA 2520 Db 2461 CCCGCAGTTCTTALCTCGACGTTTCAATAAACTATGGTTTGACAAGGTTGGTCACCA 2520	OY 2521 GTTGATAGTTACAAITTTGGGAGCAAAGGATCTCCCTTCCAGGGAAGATGGGAGGCCAAG 2580 DD 2521 GTTGATAGTTACAAITTTTGGGAGCAAAGGATCTCCCTTCCAGGGAAGATGGGAAGGCCAAG 2580	OY 2581 GAATCCTTATGTTAAGATTTACTTCCTTCCAGATAGAAGTGATAAAATAAGAGAAGAAGC 2640 DD 2581 GAATCCTTATGTTAAGATTTACTTCCTTCCAGATAGAAGTGATAAAAAAAA	OY 2641 AAAACAGTCAAGAAACTTTOGAACCCCAAATGGAACTTTCATTTTATTCTCCTGT 2700 DD 2641 AAAAACAGTCAAGAAAACTTTGGAACCCCAAATGGAACTTTCATTTTATTCTCCTGT 2700	9y 2701 CCACCCAAGAGAATTCCGTGAACGAATGCTGGAAATTACCCTTTGGGATCAAGGTAGAGT 2760 Db 2701 CCACCGAAGAGAATTCCGTGAACGAATGCTGGAAATTACCCTTTGGGATCAAGCTAGAGT 2760	Qy 2761 TCGAGAAGAGAGAGATTCTTAGGAGATTTTAATTGAATTGGAAACAGCTTTGCT 2820 Db 2761 TCGAGAAGAGAGAGCGAATTCTTAGGAGAGTTTTAATTGAATTGGAAACAGCTTTGCT 2820	QY 2821 AGATGATGACCGCACTGGTATAAGCTGCAGACCCATGATGTCTCCTCATTGCCACTCCC 2880 DD 2821 AGATGATGACGCGCACTGGTATAAGCTGCAGACCCATGATGTCTCCTCATTGCACTCCTCATTGACCTCCTCATTGACCTCCTCATTGACCACTCCTCATTGACCTCCTCATTGACCACTCCTCATTGACCTCCTCATTGACCTCCTCATTGACCTCCTCATTGACCACTCCTCATTGACCACTCCTCATTGACCACTCCTCATTGACCACTCCC 2880	OY 2881 TOGCCCTTCCCATAICTGCCCCGGAGGCAGCTCCATGGAGAGAGCCAACGCGAAGGCT 2940 DD 2881 TOGCCCTTCCCCATAICTGCCCCGGAAGCTCCATGGAGAGACCCAACGCGAGGCT 2940	OY 2941 GCAAAGGTCGAAGAATAAGTGACAGTGAAGTCTCTGACTGCACTGCGAGGATGGCT 3000 2941 GCAAAGGTCGAAGAATAAGTGACAGTGACAGAGTGTCTGACTACGACTGCGAGGATGGCT 3000	OY 3001 GGGAGTAGTGTCAGATTATCGACAATGGCCCCCGAGATCTTCAAAGGTCCACGTTGTCGGT 3060	OY 3061 GCCAGAACAAGTCATGAAATCATTGACCATCAGAGTCTCCTCATCGAGTAGA 3120 101	OY 3121 TGTTATAGGAAGGACAAGGTCATGGTCGCCTAGTGCCCCTCCTCCAAAGGAATGTGGA 3180 3121 TGTTATAGGAAGGACAAGGTCATGGTCGCCTAGTGCCCCTCCTCTCAAAGGAATGTGGA 3180	OY 3181 ACAGGGGCACCGAGGGACACGTACTAGCCATTACAACAATTAGCCGAATTGGTATGGTAGGGGATGGAT	OY 3241 ACACCOTOTICATIOACHCITCTTCAGATAGAGACAGGATTGTGAAGCAGCAGA 3300 Db 3241 ACACCGTGTCATGAGTGACCACTACTCTTCAGATAGAGAC3280	GY 3301 TAGACAGCCATATCACAGATCCAGAACAGAACAACGGCCTCTCCTAGAGCGGACCAC 3360	6y 3361 CACCCGCTCCAGATCCTCTGAACGTCCTGATACAAACCTCATGAGGTCGATGCCTTCATT 3420	3281	QY 3421 AATGACTGGAAGATCTGCCCTCCTTCACCTGCCTTATGAGGTCTCACCCTCGTACGG 3480
1261 TGITTCTTTGCQAACGCTGAACGCTGAACAACAACGAACGAACGAACGAACG	ACCATCAAGGCAAAGATCTGTATCTGAAGGTAGAGCCAATGGAAAACCAACGTTAGAGCTAAAGCAAAGATCTGTATCTGAAGGTAGAAGCTGCAATGGAAAACCAAAGATCTGTATCTGAAGGTAGAAGCTGCAATGGAAAATGAAAAATGTAAACAAAC	TTCAATGGAAAGAACTCGAGAGGCTCAGGGACAAAGTTCTTATCCACAAAGGACTCAAA	TCATAGTCCTCCCACCCCTCGGGGGGCCCTATACCGCTTGATAGACCAGACATGAGGGGGGGG	GGCTGACTCCCTACGGAAACAGCACCACTTAGATCCCAGCTCTGCTGTGAGGAAACGAA	GCGAGAAAAATGGAAACCATGTTAAGGAATGATTCTTTGAGTTCAGACCAGTCCGAGTC				MAAAG	GANGTACTATGGTGGCCACTCTTTGGAAGGATTTTGGAATGGTCTGAGCCTCAGATTAA	GGACTCTGGGGTAGATACCTGTAGTAGACACCCTTAACGAGGGGTAGCCATAGTGA 	TAAGGA.CCCTGTGA.CCTGGCAGCCATCCAAAGATGGAGATCGCCTAATTGGTCGTGTTTTTTTT		AAAGGTISTAGGAGAAAGATGACTGAATCAGGTCGACTTTGTGCATTTATTACCAAAGT 	AAAAAAAGGAAGTTTAGCTGATACTGTAGGACATCTTAGACCAGGTGATGAAGTCTTGGA	2221 ATGEAATGGGAGGCTATTGCAAGGAGCCACATTGAGGAAGTTACAACATTATATAGA 2280	2221 ATGGAATGGGAGCTATTGCAAGGAGCCACATTTGAGGAAGTTTACAACATTATTCTAGA 2280 2281 ATTCRAAACTTGAAACTACAAGGTTTCAAGTTTTCAAAGTTAACAAATTAAAAAGAATTAAAAAAAA	ATCCAAACCTGAACCACAAGTTGAGCTTGTTTCAAGGCCAATTGGAGATATTCCTAG	2341 AATACCTGATAGCACGCATGCACAACTGGAATCCAGTTCTAGCTCATTTGAATCTCAAAA 2400

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Wang, Y. and Sudhof, T.C.
Wang, Y. and Sudhof, T.C.
Submitsed (27-007-1999) Center for Basic Neuroscience, The
University of Texas Southwestern Medical Center, 6000 Harry Hines
Blvd., Dallas, TX 75235-9111, USA
Location/Qualifiers
1. .5550
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The RIM/NIM family of neuronal C2 domain proteins. Interactions with Rabs and a new class of Src homology 3 domain proteins J. Biol. Chem. 275 (26), 20033-20044 (2000) Rattus norvegicus (Norway rat) AF199331.1 GI:8925875 Rattus. 1 (bases 1 to 5550) 4681 DEFINITION ACCESSION VERSION KEYWORDS SOURCE source ORGANISM REPERENCE AUTHORS AUTHORS TITLE TITLE gene REFERENCE JOURNAL e FRATURES AF199331 ò ò 셤 ઠ ò

SDPWIARYPVKPOPYBEOMRIHAEVSRARHERRHSDVSLANAELEDSRISLLENDRPE
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1281 C 1388 G 1218 C

Gaps Query Match 78.0%; Score 3886; DB 10; Length 5550; Best Local Similarity 88.0%; Pred. No. 0; Matches 4443; Conservative 0; Mismatches 275; Indels 332; ठ

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Mang, Y. and Sudhof, T.C.
Mang, Y. and Sudhof, T.C.
Mang, Y. and Sudhof, T.C.
Submitset Submission
Submitted (27-OCT-1999) Center for Basic Neuroscience, The
University of Texas Southwestern Medical Center, 6000 Harry Hines
Blvd., Dallas, TX 75235-9111, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                             Rattus norvegicus
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae,
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1 (bases 1 to 5592)

Wang, T., Sugita, S. and Sudhof, T.C.
The RIM,NIM family of neuronal C2 domain proteins. Interactions with Rab3 and a new class of Src homology 3 domain proteins
J. Biol. Chem. 275 (26), 20033-20044 (2000)
                                                                                                                                                                                         AF199330 5592 bp mRNA linear ROD Rattus norvegicus RIM2-5A (Rim2-5A) mRNA, complete cds.
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GAACTTGACCAAAAGCACCAGCATCAGTGGAGACATGTGCTCCACTGGAGAAAAAAGGG 3954
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                                                                                                                        CAGCCAGTCCGACACTGCAGTGGGCGCCCTGGGTACCAGTGGCAAGAAGCGGCGATCTAG
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Db 921 TTTAAATTATAGGGATTCTAACAGGAGGCCALAGACATTCCAAAGAGTATATTGTAGA 980	Oy 1081 TGATGAAGATGTGGAGACAGAGATATGAATATGAAAGACAAAGAGAGAG	OY 1141 OGCACGCTACAGAAGTGATCCAAATCTGGCCCGGTATCCCGTAAAGCCACAACCCTACGA 1200 DD 1041 GGCACGCTACAGAAGTGATCCAAATTTGGCCCGGTATCCGGTAAAGCCACAAACCTATGA 1100	Oy 1201 AGAACAAATGCGCATCCACGCTGAGGTGTCCAGGGCACGACATGAGAGGCACAGTGA 1260	Oy 1261 IGTTCTTTGGCAAACGCTGAACTAGAAGATTCCAGGATTTCTCTGCTAAGGATGGAT	OY 1321 ACCATCAAGGCAAAGATCTGTATCTGAAGGTAGGGCTGCAATGGAAACCAACGATGGTA 1380	OY 1381 TTCAATOGAAAGAACTCGAGACGACAAAGTTCTTATCCACAAAGACCTCAAA 1440 Db 1281 TTCAATOGAAAGAACTCGAGAAAGTCTCAGAGAAGTTCTTATCCACAAAGACCACAAA 1340	OY 1441 TCATAGTCCTCCCCCCCTCGGGGGGGGCCCTATACCGCTTATAGACCAGACATGAGGG 1500 1341 TCATAGTCCTCCTACCCCTCGGAGGGCCCTATACCGCTCGATAGACCAGAGCTGAGGGG 1400	OY 1501 CGCTGACTCCCTACGGAAACACCACTTAGATCCCAGCTCTGCTGTGAGGAAAACGAA 1560 Db 1401 TGCCGACTCCCTACGGAAACAAACACACTCTTAGATCCCAGCTCTGCTGTAAGGAAAACGAA 1460	Oy 1561 GCGAGAAAAATGGAAACCATGTFAAGGAATGATTCTTTGAĞTTCAGACCAGTCCGAGTC 1620 Db 1461 GCGAGAAAAAATGGAAACAATGATTGAGGAATGATTCTTTGAGTTCAGACCAGTCTGAGTC 1520	Oy 1621 AGTGAGGCCCCCACCAGGGCCTCATAAATCCAAGAAGGGGTAAAATGCGCCAGGT 1680 1521 AGTGAGGCCGCCCCACCAGGGCCTCATAAATCCAAGAAGGAGGTAAAATGCGCCAGGT 1580	1681	1741	1801 AACTAGTGAGCAGGAGTTTTGTCGGGATTCTAACAGGTCTGAGAGAAAGAA	OY 1861 GAIGHACHAIGENGECCACTCTHTGGAAGAHTHTGGAATGACGAGGATTAA 1920 Db 1682	1921 GANCTCTGGGGTAGATACCTGTAGTAGCACACCTTAACGACGATAGCCATAGTGATAGTGTAGTGTAGTGTGTGT	1981 TAAGARCCCTGTGACCTGGCAGCCATCCAAGATGGAGTTGAATTGGTGGTGATTTTTTTT	OY 2041 ATTAAATAAGCGTTTAAAGATOGGAGTGTACCTCGAGAATCTCAGAAGCAATGCTGGGCTT 2100	Qy 2101 AAAGGTTGTAGGAAGGAAAGATGACTGAATCAGGTCGACTTTGTGCATTTATTACCAAAGT 2160
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TITLE Direct Submission JOURNAL Submitted (27-OCT-1999) Center for Basic Neuroscience, The University of Texas Southwestern Medical Center, 6000 Harry Hines Blvd., Dallas, TX 75235-911, USA FRATURES FRATURES Jocation/Qualifiers 1.5640 1.5640	/gene="#im2" /codon_start=1 /product="RIN2" /protein_id="AAP81644.1" /protein_id="AAP81644.1" /protein_id="AAP81644.1" /protein_id="AAP8164FRIPAABQPPPQPEMPDLASHLTERERKIIQANM / translation="MARAHGAPRAPAPAABQPPPQPEMPDLASHLTERERKIIQANM DROKKEEKEGGVLKTCHAQOPEMTKEGVKOMGKESQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQ	ROUGHLANT PUNCHONT RECORD THAN TROUGHES AT 1 VOIDED VERGING TERCORDERS TO AND AND AND AND AND AND AND AND AND AND	PROGRAVE STATEMENT STATEME	BASE COUNT 1695 a 1301 c 1409 g 1235 t ORIGIN Query Match Best Local Similarity 86.4%; Fred. No. 0; Matches 4443; Conservative 0; Mismatches 275; Indels 422; Gaps 8;	
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Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae;
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Wang, Y. and Sudhof, T.C.
Direct Submission
Submitted (30-SER-2002) Center for Basic Neuroscience, The
University of Texas Southwestern Medical Center at Dallas, 6000
Harry Hines Blvd, Dallas, TX 75390, USA
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Wangy: and Sudhof, T.C.
Genomic definition of RIM proteins: evolutionary amplification
family of synaptic regulatory proteins
Genomics 81 (2), 126-137 (2003)
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Page 19	1770 GARGOLANGGARTTCCTTCCGGGGGGGGGGGGGGGAACCCAAGAACCCGGGGGGGG
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SDPNLARYPVRQDPFEGWRITHEVSRARHFRHSDVSLANAELEDSRISILLRWDRPS
RQRSYSBRRAAMENGRSYSWERTREAQSQSSYPQRTTWHSPPTPRRSPILDERELADRS
ADSLRKQHHLDPSSAVRKTKREKMSTMLRNDSLSSDQSESVRPPPPRPHKSKKGGGWR
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AP199324.1 GI:8925861
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Mang X. and Sudhof, T.C.
Direct Submission
Submitted (27-OCT-1999) Center for Basic Neuroscience, The
University of Faxas Southwestern Medical Center, 6000 Harry Hines
Blvd., Dallas, TX 7553-59111, USA
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Sattus norvegicus
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae;
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The RIM/NIM family of neuronal C2 domain proteins. Interactions with Rab3 and a new class of Src homology 3 domain proteins J. Biol. Chem. 275 (26), 20033-20044 (2000)
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RPMLEITLMDQARVREEESSFLGEILIELETALLDDEPHWYLCGTHDVSSLFPPPSF
KOLPSFREGGSFRIAGNSTRIBENSTOCHDGVGWVBDYRHDGRDLGSSTLEPPSF
YMPRRQLAGSSFRADTRIAGRSKAISSENTGYBEHHBDGROCKAADDGYPHRSESTERQRPLL
RRYTTRSRSSERADTRIAGRSKAISSPRIAGRSPPSPSPSTORY
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SSEGRIL FPGYLLEDSGSPPLDGLGPAQUVGROTLATPAMOSICOLEV
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Mammalia, Butheria, Rodentia, Sciurognathi, Muridas, Murinas,
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The RIM/RIM family of neuronal C2 domain proteins. Interactions
with Rab3 and a new class of Src homology 3 domain proteins
J. Biol. Chem. 275 (26), 20033-20044 (2000)
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Best Local Similarity 79.0%; Pred. No. 0;
Matches 3938; Conservative 0; Mismatches 261; Indels 785; Gaps
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Rattus norvegicus RIM2-4C (Rim2-4C) mRNA, complete cds.
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae,
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Wang,Y., Sugita,S. and Sudhof,T.C.
The RIM/NIM family of neuronal C2 domain proteins. Interactions with Rab3 and a new class of Src homology 3 domain proteins J. Biol. Chem. 275 (26), 20033-20044 (2000)
                      AACCAAGGTGGCGAGAAAGACGCTGGGAGCCCCTGTATCAGCAGCTGTTATCTTTCGAAGA
                                                                                                                                                                                                                                                                            GACAAGAAGAAGCTTCCCCAATCGTCTGGAAAGTTCTACTACTGGACCTTCTTACTCTGGTTC
                                                             GAGCCCCCAGGGGGGGGGTGTTACAGATCATTGTCTGGGGGAGATTATGGTCGTATGGATCA
                                                                                           3801 GAGCCCCCAGGGGAAGGTGTTACAGATCATTGTCTGGGGAGATTATGGCCGCATGGATCA
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Wang, Y. and Sudhof, T.C.
Direct Submission
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Rattus norvegicus RIM2-3B (Rim2-3B) mRNA, complete cds.
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Sattus norvegicus (Abrakas)
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Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae,
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The RIM/NIM family of neuronal C2 domain proteins. Interactions
with Rab3 and a new class of Src homology 3 domain proteins
J. Biol. Chem. 275 (26), 20033-20044 (2000)
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	3241 ACACCGTGTCATGACCACTACTCTTCAGATAGAGC	3060 TCGCTCTCGACACACACACACAGTCACCACCACACAGGGATGGAAGC 3119 3295 AGCAGATAGACACCATATCACAGATCCACACACACACACA	ATGCC	3415 TTCATTAATGACTGGAAGATCTGCCCTCCTTCACCTGCCTTATCGAGGTCTCACCCTCG 3474	3475 TACCGGGTCTGTCCAGACAAGCCCATCAAGTACTCCGGGAACAGGACGAAGGGGCCGACA 3534	3535 GCTTCCACAGCTTCCACCAAAGGGAACATTCGAGAAAGTGCTATGGATATAGAGAĞAG 3594		GCAAGATTACCATTCGAAGTATCGCTCAGGATGGGATCCACATAGAGGGGCAGATACTGT	TTCCACTAAATCCTCGGACAGTGATGTAAGTGATGTATCTGCGGTTTCAAGGACTAGTAG	TCTCGTTTCAGCAGACACAAGCTACATGTCCGACCAATCAGAGCGGCCGAGAGGAAA	CAGGAAAATCAGTGTCTTTACATCCAAAATGCAAAACAGACAG	3395 GAACTTGACCAAAAGCACCAGCATCAGTGGAGACATGTGCTCACTGGAGAAGAATGACGG 3954 3396 3395	CAGCCAGTCCGACACACAGTGGGCCCTGGGTACCAGTGGCAAGAAGCGGCGATCTAG	CATTGGGGCCAAAATGGTAGCTATTGTTGGTCTCTCACGGAAAAGTCGCAGTGCCTCTCA	3359	4135 GACCGGGCTAGCAGTGGAGATGAGGAACTGGATGACCGCGAGGCCAGCCGGGAATCCAC 4194

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Mangy. and Sudhof.T.C.
Direct Submission
Submitted (27-OCT-1999) Center for Basic Neuroscience, The
University of Texas Southwestern Medical Center, 6000 Harry Hines
Blvd., Dallas, TX 7525-5911, USA
Location/Qualifiers
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Wang Y. and Sudhof,T.C.
Direct Submission
Submitted (27-007-1999) Center for Basic Neuroscience, The
University of Texas Southwestern Medical Center, 6000 Harry Hines
Blvd., Dallas, TX 75235-9111, USA
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The RIM/NIM family of neuronal C2 domain proteins. Interactions
with Rab3 and a new class of Src homology 3 domain proteins
J. Biol. Chem. 275 (26), 20033-20044 (2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21 GCTTCCCTAGGGTGGTTCGGCTCCACCAAGCATGTCGGCTCCACTCGGGCCCCGGGGCCCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CCCGGCTCCCACCCCGGCGGCCTCTCAACCTCCGCAGCAGCAGATGCCGGACCTCAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -- AAAGCTGCATCAACAATTTGAAATGTATAAGGA
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GCGAGAAAAATGGAAACAATGTTGAGAATGATTCTTTGAGTTCAGACCAGTCTGAGTC AGTGAGGCCGCCCCACCACCACCACCACATAAATCCAAGAAAGGAGGTAAAATGCGCCACGT HIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	1521 AGTGAGGCCGCCCCCCCCCCCTCATAATCCCAGAAAGGGGGCGCGGGT 1580 1681 TTCACTGAGCGCCTCGGAGGAGGAGGAGCATCCACACCTGAGTATACAAGCTGTGATA 1740 1581 TTCACTGAGCAGCTCGAGGAGGAGGTGCACCTCCACGCCTGAGTATACAAGCTGTGATGA 1740 1581 TTCACTGAGCACTCCAGAGGAGTTGGCATCCACGCCTGAGTATACAAGCTGTGATGA 1640	1741 TGTOGAGCTOGAAAGCGAGAGTGTGAGTGAGAGGGGAAGTGAAAAGGGAAAAAAA 1800 	1861 GATGTACTATGGCCACTCTTTGGAAGGATTTGGAATGGCCTGAGCCTCAGATTAA 1920	1921 GGACTCTGGGGTAGTACTGTAGTAGCACCCTTAACGAGGAGCATAGTGA 1980 1713 G	1740 TTTGCACCCTGTGACCAGCCACCCATCCAAGATGGAGATCGCCTAATTGGTCGTATTT 1799 2041 ATTAAATAAGGGTTTAAAAGATGGGAGTGTACCTCGAGACTCAGGAGCAATGCTGGCTT 2100 1800 ATTAAATAAGCGTTTAAAAGATGGGAGTGTACCTGGAGATCCAGGAGCAATGCTGGGCTT 1859	2101 AAAGGTTGTAGGAGAAAAGATGACTGAATCAGGTCGACTTTGTGCATTTATTACCAAAGT 2160 		AUGGARIGGGRGETATIGCARGGRGECACATTIGRGGARGITTACACATATTICTAGA AIGGBAIGGAAGGCIATTGCAGAGGCCACATTIGRGGAAGTTTACAACATTATCIAGA AIGGBAIGGAAGGGAAGGGAGCCACATTIGRAGGAAGTTTACAACATTATTATTATTATTATTATTATTATTATATATTAT	2341 AATROCTGATGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	AATACCIGATAGCACTCATGCACAACTGGAATCCAGTTCTAGCTCATTTGAATCTCAAAA	AATGGATCGTCCGTCTATATCGGTACCTCTCCCATGAGTCCTGGCATGCTGAGGGATGT	CCCGCAGTICTIAICTICAGCACACTTICAATAAACTAIGGTTGACAAGGTTGGTCACCA CCCACAGTICTTATCTGGACAGCTTTCAATAAACTATGGTTTGACAGGTTGGTT	2521 GITGATACTACAATTTTGGGAGCAAAGGATCTCCCTTCCAGGGAAGTTGGGAGGCCAAG 2580 2280 GITAATAGTTACAATTTTGGGAGCAAAGGATCTCCCTTCCAGGAAAATGGGAGGCCAAG 2339	2581 GAATCCTTATGTTAAGATTTACTTCCTTCCAGATAGAAGTGATAAAAAAAA	2641 AAAAACACTCAAQAAAACTTTGGAACCCAAATGGAACCAGACTTTCATTTTATTCTCCTGT 2700
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481 TTGCCAAACCAAGTTCTGTGCTCGATGTGGAGGTCGAGTGTCTTTACGCTCGAAACAAGGT 540	441 TATGICGGTGTTTTTTTGTGCCGAAACAAGAATCCTCACTAGTTTTTTTT	661 TCGAAATGAGGAAGCCCTCAGGAGAAGGAAAACTACACGAGCAGCCCCAGTTCCA 720	GGGACCCCCGGTGACTCATCAGTACCTGCAGTTGAGAGAGGTCGAGCTCATGGGCTCAC AAGACAGGATACTATTAAAAATGGATCAGGAGTGAAGCACCAGATTGCCAGTGACATGCC AAGACAGGATACTATTAAAAATGGATCAGGAGTGAAGCACCAGATTGCCAGTGACATGCC AAGACAGGATTCTATTAAAAATGGATCAGGAATGAAATGAAATGGAATGGCCAAGAATGGCAAGAATGGCCAAGAATGGCCAAGAATGGCCAAGAATGGCCAAGAATGGCCAAGAATGGCAAGAATGGCAAGAATGGCAAGAATGGCAAGAATGGCAAGAATGGCAAGAATGGCCAAGAATGGCAAGAATGGCAAGAATGGCAAGAATGGCAAGAATGGCAAGAATGGCAAGAATGGCCAAGAATGGCAAGAATGGCAAGAATGGCAAGAATGGCAAGAATGGCAAGAATGGCAAGAATGGCCAAGAATGGCAAGAATGAAATG	841 TTCAGACAGAAAACGAAGTCCATGTCCCAGGGATCAAAATCGAAGATACGAGCAAAG 900 741 TTCAGACAGAAAAGAAGTCCGTCAGTGTCCCAGGGATCAAAATCGAAGATACGACCAAAG 800 901 TGAAAAAAGAAAGAAGACTACTACAGTATTCCTTCAGATGTTACAAAGCAAATCCC 960	TGAAGAAAGAAAGAAATATTCACATGCTTCCAGATAGCACAATGCCTAGATCTCC TTCGGATTATGCTGATAGCGATCCTCCAGATTATATGAAGAACCTGGTCA TTCGGATTATGCTGATAGACGATCTCAGCGTGAGCCTCAATTTTATGAAGAACCTGGTCA	861 AICAGAITAIGCIGAITAGACGAITCICAACGIGAACCICAATITIAIGAAGAACCIGAITA 920 1021 ITTAAAITACAGGAITCITAACAGGAGAGGCCATAGACATTCCAAAGAGTATATTGTGGA 1080 1021 ITTAAAITATAGGGAITCTAACAGGAGAGGCCATAGACATTCCAAAGAGTATATTGTAGA 980	1081 TGATGAAGATGTGGAGAGCAGAGATGAATATGAAAGACAAAGGAGGAGGAGGAATACCA 1140 	1141 GGCACGCTACAGAAGTGATCCAAATCTGGCCCGGTATCCCGTAAAGCCACAACCCTACGA 1200 		1261 TGTTTCTTTGGCAAACGCTGAACTAGAAGATTCCAGGATTTCTCTGCTAAGGATGGAT	1321 ACCATCAAGGCAAAGATCTGTATCTGAACGTAGAGCTGCAATGGAAAACCAACGATGGTA 1380 	1381 TICAANGGAAAGAACTCGAGAGGCTCAGGGACAAAGTICTTATCCACAAAGGACCTCAAA 1440 	1441 TCATAGTCCTCCCTCGGCGGGGGCCCTATACCGCTTGATAGGCGGCAGACATGAGGCG	CGCTGACTCCCTACGGAAACACCACCTTAGATCCCAGCTCTGCTGTGAGGAAAACAA	GCGAGAAAAATGGAAACCATGTTAAGGAATGATTCTTTGAGTTCAGACCAGTCCGAGTC

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3781 TCGTTTCAGCAGCACAAGCTACATGTCCGTCCAATCAGAGGGGCCGAGAGGAAACAGGAA 3840	3216		GACCAAAAGCACCAGCATCAGTGGAGACATGTGCTCACTGGAAAAAAATGACGGCAGCCA	3961 Grocalactecagroscoccrossances 4020	GGCCAAAATGGTAGCTATTGTTGGTCTCTCAGGAAAAGTGGCAGTGCCTCTCAACTCAG	CCAAACCGAAGGAGGTAAAAAGCTACGAAGCACTGTTCAGAGAAGCACGGGGACCGG	4141 GCTAGCAGTGGAGATGAGAACTGGATGACCGGCGAGGCCAGCGGGGGGAATCCACGGATGG 4200 3267 GCTAGCAGTGGAGAAGGAACTGGATGACAAGACCGAGACCGGGAATCCACGGAATGG 3326	4201 CAGCATGAACAGCTTATAGCTTCGAAGGAAATCTGATCTTCCTTC	4261 TGACAGCCAGTTCAGTGATTTCCTGGATGGCCTGGGCCCTGCTCAGCTAGTGGGACGCCA 4320 3387 TGACAGCCAGTTCAGCGATTTCCTTGATGGTCTGGGCCCTGCTCAGCTAGTGGGACCCA 3446	4321 GACCTGGCTACTCCTGCAATGGGTGACATTCAGGTGGAATGATGGATAAAAGGGACA 4380 3447 GACCCTGGGGACTCCTGCAATGGGTGACATTCAGGTGGGGAATGATGGATG	4381 GCTGGAGGTAGAAATCATCCGGGCGCGCGCGCTTGTGGTAAAACCAGGTTCCAAGACACT 4440 3507 GCTGGAGGTCGAGGATCGTCCGGGGTCCGAGGCCTTGTAGTAAAACCAGGTTCCAAGACAT 3566	4441 GCCAGCACGTATGTCAAGGTGTATCTGTTAGACAAGGAGTCTGCATAGCCAAAAGAA 4500	AACCAAGGTGGCGAGAAAGACCCTGGAGCCCTGTACCAGCAGCTCTTGTCCTTCGAGGA	GAGCCCCCAGGGGAGGTGTTACAGATCATTGTCTGGGAGATTATGGTGTATTGGATCATATGGATCATATGGATCATATGGATCATATGGTGTTACAGATCATTGTTGTCTGGGGAGATTATGGCCGCATGGATCATTGTTGTCTGGGGAGATTATGGCCGCATGGATCATTGTTGTCTGGGGAAGATTATGGACCGCATGGATCATTGTCTGGGGAAGATTATGGACCGCATGGATCATTGTCTGGGGAAGATTATGATCATTGTCTGGGGAAGATTATGATCATTGATCATTGATCATTGATCATTGATCATTGATTG		4681 GATTGGATGGTTCAACTCTTCCCTCCTCCTCTCCTCTAGAATCCAACCTCGGCACCTCT 4740 3807 AAITGGATGGTTCAAACTCTTCCCTCCTTCCTCCCTAGTAGATCCAACCTTGGCACCTCT 3866	4741 GACAAGAAGACTTCCCAATCGTCTCTGGAAAGTTCTACCGGACCTTCTTACTCTTGTTC 4800	4801 ATAGCAACTATAAAACTGTTGTCACAACCAGCGATACGAAAACCAGAGAAACGCA 4860
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2400 AAAAACAGTCAAGAAAACTTTGGAACCCAAATGGAACCAGACTTTCATTTATTCTCCTGT 2459 2701 CCACCGAAGAGAATTCCGAGAAAGGAATGCAAAATTACCCTTTTAGAGATTAGAGT 2760	TCACCGAAGAGATTCCGGGGAACGGAATGCTCGAAATCACCCTTTGGGATCAAGCTCGAGT	2761 TCCAGAAGAGAGCGAATTCTTAGGAGATTTTAATTGAATTGGAAACAGCTTTGCT 2820 	2821 AGATGATGAGCCGCACTGGTATAAGCTGCAGACCCATGATGTCTCCTCATTGCCACTCCC 2880 2580 AGATGATGAACGACACTGGTACAAACTTCAGACCCATGATGTCTCCTCATTGCCACTCCC 2639	2881 TCGCCCTTCCCCATATCTGCCCCGGAGGCAGCTCCATGGAGAGACCCCAACGCGCAGGCT 2940 2640 TCGCCTTCTCCATATATGCCACGGAACAGCCCAAGAGAGCCCAACACGCAGGTT 2699	2941 GCAAAGGTCGAAGAATAAGTGACAGTGAAGTGTCTCGACTACGACTGCGAGGATGGCGT 3000 	3001 GGGAGTAGTGTCAGATTATCGACACAGAGCCCGCGATCTTCAAAGCTCCCACGTTGTCGTT 3060 	3061 GCCAGAACAAGTCATGAAATCATTGCTCACCATCAGGGTCTCCTCATCGAGTAGA 3120 	3121 TGTTATAGGAAGAACAAGGTCATGGCCTAGTGCCCCTCCTCCTCCAAAGAAAG		3241 ACACCGTGTCATGGATGACCACTACTCTTCAGATAGAGACAGGGATTGTGAAGCAGCAGA 3300 3000 ACACCGTGTCATGAGGACCACTATTACTCTTCAAGAGAGAG		Grcgargcctrcart	AATGACTGGAAGATCTGCCCTCCTTCACCTGCCTTATCGAGGTCTCACCCTCGTACCGG	3481 GTCTGTCCAGACAACCCATCAAGTACTCCGGGAACAGACGACGACGACAGACA		AGCAAGA	TTACCATTCGAAGTATCGCTCAGGATGGGATCCACATAGAGGGGCAGATACTGTTTCCAC	3716

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                            - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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1: /SIDS1/qcqdata/q
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Maximum DB seq length: 200000000
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                                                                                                                                                       OM nucleic
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Mouse Rim2-encodin	Human secreted pro	Human neuroblastom	Human DNA sequence	Human secreted pro	Human nervous syst	EST clone DM118.	EST clone CO618.
SUMMARIES	ជ	AAF86684	AAV40485	AA198097			ABA11415		AAV89630
	BB	22	13	22	7	21	22	20	20
	Query e Match Length DB I	4980	1302	6637	7325	2276	526	355	355
*	Query	100.0	17.0	14.4	8.0	7.6	6.4	4.2	4.2
	Score	4980	844.8	715	398.2	377	318.8	207.6	207.6
	Result No.	-	N	м	4	ഹ	9	0	œ

	Buren ORFX ORF489	Drosophila melanod	Human breast cell	Ruman fostal liver	#4068 £	brain			4276	#4036		Human denome-deriv	Rat BST-derived co	Human breast cell	Probe #14901 for g	Human brain expres	Human bone marrow	Probe #18328 used		Human liver single	Human genome-deriv	Movel murine polyn	Drosophila melanog	Human breast cell	Ruman foetal liver	Probe #13970 for g	Human brain expres	Ruman bone marrow	Probe #13348 for g	Probe #17421 used	Probe #9032 used t	Human liver single	Human genome-deriv	Mouse spliced tran	Drosophila melanoq	Human Docz-beta ge	Human breast cell
	AAC74934	ABL12715	ABA45437	ABA55935	ABA25602	AAK04148	AAX29630	AAI14209	AAI35590	AAI04045	ABS29267	ABS04186	AAH98466	ABA51486	ABA36435	AAK17764	AAK43584	AAI49642	AAI09911	ABS43229	ABS17744	ABS69183	ABL12714	ABA50565	ABA68523	ABA35504	AAK16890	AAK42661	AAI23415	AAI48735	AAI09041	ABS42283	AB816713	ABN54404	ABL12699	AAT79627	ABA46385
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	3.9	3.8	2.3	2.3	2.3	2.3	2.3	2.3	2.3	2.3	2.3	2.3	2.5	1.6	1.6	1.6	1.6	1.6	1.6	1.6	1.6		1.4	1.4	1.4	4	7.4	7.7	7.4	1.4	1.4	7.7	1.4	1.3	1.3	1:1	1:1
	195.6	188.8	113.8	113.8	113.8	113.8	113.8	113.8	113.8	113.8	113.8	113.8	111.4	80.4	80.4	80.4	80.4	80.4	80.4	80.4	80.4	76.8	72.2	8.69	69.8	69.8	8.69	69.8	90.00	69.8	69·B	69.8	69.B	65	63	55.4	54.4
	O	ដ	7	12	13	14	15	16	11	18	13	50	21	75	23	77	52	56	27	78	53	30	31	35	33	34	9	9 1	7	38	39	40	41	42	43	44	45
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ALIGNMENTS

RESULT 1

Mouse; murine; Rim2; Rim isoform; Rab3-interacting molecule; Rab3-dependent intracellular vesicle fusion regulator; dependent intracellular vesicle fusion regulator; dependent intracellular vesicle fusion regulator; exocytosis; hormone secretion; neurotransmitter release; presynaptic membrane; neuropathy; central nervous system disorder; brain disorder; secretion disorder; pituitary gland; hypothalamus; pancreatic beta-cell; diabetes; parotid gland; zinc finger; FDZ domain; AAF86684 standard; cDNA; 4980 25-JUL-2001 (first entry) Mouse Rim2-encoding cDNA. C2 domain; ss Mus musculus AAF86684;

Location/Qualifiers
32.4804
Atags a "Actags "Mouse Rim 2"
/producs "Rim 2 is a novel isoform of Rim"

BP1090986-A1

11-APR-2001.

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PF 31-JUL-2000; 2000EP-0116148.

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(JCRP-) JCR FHARM CO LTD.

PA (SEIN/) SEINO S.

XX
XX

WPI; 2001-275168/29.

P-PSDB; AAB73488.

XX
WPI; 2001-275168/29.

PR PRASS and mucleic acids encoding the protein useful in diagnosing endocrine-related diseases or neuropathy and in developing process of the prevention or treatment of such diseases.

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New Rim 2 proteins and mucleic acids encoding the protein useful in diagnosing endocrine-related diseases or neuropathy and in developing process for the prevention or treatment of such diseases.

XX
XX

This sequence represents cDNA encoding mouse Rim2. Rim2 is a novel septification as Rim1), and both proteins contain a zinc finger, pre-related two c2 domains. Rim2 is able to specifically interact with cc pecification as Rim1), and both proteins contain a zinc finger, pre-related to be a requistor of Rab3-dependent intracellular vesicle is believed to be a requistor of Rab3-dependent intracellular vesicle contourine-related diseases or neuropathy and in developing agents for contourine-related diseases or neuropathy and in developing agents for the prevention or treatment of such diseases. Rim2 specific membranes, and in hormonal secretion. The Rim2 protein is useful in the diagnosing cc the prevention probes or antibodies are useful in the diagnosis of brain cc or central nervous system disorders, or for diagnosis of brain and parotid gland.

XX
Sequence 4980 BP; 1503 A; 1161 C; 1282 G; 1034 T; 0 other:
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SQ Sequence 4980 BP; 1503 A; 1161 C; 1282 G; 1034 T; 0 other;
Query Match
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4980; Conservative 0; Mismatches 0; Indels 0; Gag

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1200 1080 1260 1320 1380 1380 1500 TTCGGAITATGCTGATAGACGATCTCAGCGTGAGCCTCAATTTATATGAAGAACCTCGGTCA 1020 TITAAATTACAGGGATTCTAACAGGAGGCCATAGACATTCCAAAGAGTATATTGTGGA 1080 GCCACGCTACAGAAGTGCAAATCTGGCCCGGTAATCCCGTAAAGCCACAAACCTACGA 1200 CGCTGACTCCCTACGGAAACAGCACCACTTAGATCCCAGCTCTGCTGAAGGAAAACGAA 1560 GCGAGAAAAATGGAAACCATGTTAAGGAATGATTCTTTGAGTTCAGACCAGTCCGAGTC 1620 TTCGGATTATGCTGATAGACGATCTCAGCGTGAGCCTCAATTTTATGAAGAACCTGGTCA 1020 AGAACAAATGCGCATCCACGCTGAGGTGTCCAGGGCACGACATGAGAAAAGACACAGTGA 1260 TTCAATGGAAAGAACTCGAGAGGGCCAAAAGTTCTTATCCACAAAAGGACCTCAAA 1440 TTCAATGGAAAGAACTCGAGAGGCTCAGGGACAAAGTTCTTATCCACAAAAGGACCTCAAA 1440 481 TIGCCAAACCAAGTTCTGTGCTCGATGTGGAGGTCGAGGTTTTACGCTCAAACAAGGT 540 660 TGAAGAAAGAGAGAGTACTCACAGTATGTTCCTTCAGATGGTACAATGCCAAGATCTCC 960 TATGROGETGTGTATTTGTGCCGAAAACAACAAGAAATCCTCACTAAATCAGGAGCATG 600 660 720 721 AGGAGCCCCAGGTGACTTATCAGTACCTGCAGTTGAGAAAGGCCGAGCTCATGGGCTCAC 780 780 840 840 TTCAGACAGAAACGAAGTCCATCAGTGTCCAGGGATCAAAATCGAAGATACGAGGCAAAG 900 900 GITITATAATAGIGGGTCTAACACACTGCAGCAACCTGATCAAAAGGTTCCTCGAGGGGCT TCGAAATGAGGAAGCCCCTCAGGAGAAGAAAGTAACTACAGGAGCCCCCAGTTCCA 721 AGGAGCCCCAGGTGACTTATCAGTACCTGCAGTTGAGAAAAGGCCGAAGCTCATGGGCTCAC 781 AAGACAGGATACTATTAAAATGGATCAGAAGTGAAGCACCCGAGATTGCCAGTGACATGCC 841 TTCAGACAGAAAACGAAGTCCATCAGTGTCCAGGGATCAAAATCGAAGATACGAAG TITAAATTACAGGGATTCTAACAGGAGGCCATAGACATTCCAAAGAGTATATTGTGGA GGCACGCTACAGAAGTGATCCAAATCTGGCCCGGTATCCCGTAAAGCCACAACCCTACGA 1201 AGAACAAATGCGCATCCACGCTGAGGTGTCCAGGGCACGACAAGAGAAAGGCACAGTGA TCATAGTCCTCCCCCCCCCCCCGGGGGCCCTATACCGCTTGATAGACCGCGCG CGCTGACTCCCTACGGAAACAGCACCACTTAGATCCCAGCTCTGCTGTGAGGAAACGAA GITITIATAATAGIGGGICTAACACACIGCAGCAACCIGATCAAAAGTITCCICCAAGGCI TCGAAATGAGGAAGCCCCTCAGGAGAAGAAAGCAAACTACACGAGCCGCCCCAGTTCCA AAGACAGGATACTATTAAAAATGGATCAGGAGTGAAGCACCCAGATTGCCAGTGACATGCC TGAAGAAAGAGGACTACTCACAGTATGTTCCTTCAGATGGTACAATGCCAAGATCTCC **ACCATCAAGGCAAAGATCTGTATCTGAACGTAGAGCTGCAATGGAAAACCAAGGATCGTA** 1321 ACCATCAAGGCAAAGATCTGTATCTGAACGTAGAGCTGCAATGGAAAACCAAACGTAACTTA TCATAGTCCTCCCACCCTCGGCGGAGCCCTATACCGCTTGATAGACCAGACATGAGGCG 1021 1201 1261 1381 1441 541 541 661 781 901 961 1021 1081 1081 1141 1141 1261 1321 1381 1441 1501 1501 1561 601 109 661 841 901 961 à 윱 ò ð B ò 윰 Š 8 ò 윰 ò 윱 ò 윱 ò ద ò ద à 吊 ò 셤 ð 셤 Š 윱 8 셤 à 유

OY 2701 CCACCGAAGAATTCCGTGAACGAATGCTGGAAATTACCCTTTGGGATCAAGCTAGAGT	2761	2821	2881	OY 2941 GCAAAGTCGAAGAGAATAAGTGACAAGTGAAGTGCTGACTACGACTGCGAGGATGGTGTGTGT	OY 3001 GGGAGTAGTGACATTATCGACACAATGGCCGCGATCTTCAAAGCTCCACGTTGTCGGT 3001 GGGAGTAGTGTCAAATATCGACACAATGGCCGCGATCTTCAAAGCTCCACGTTGTCGGT	Oy 3061 GCCAGAACAACATCATCACAAACATTGCTCACCATCAGGGTCTCCTCATCGAGTAGA	Qy 3121 TGTTATAGGAACAAGGTCATGGTCGCCTAGTGCCCTCCTCCTCAAAGGAATGTGGA Db 3121 TGTTATAGGAACAAGGTCATGGTCGCCTAGTGCCCTCCTCCAAAGGAATGTGGA	OY 3181 ACAGGGCACCGAGGGACACGTGCTACTGGCCATTACAACAATTAGCCGAATTGGTTGG	Oy 3241 ACACCTCATGGATGACCACTACTCTTCAGATAGAGACAGGATTGTGAAGCAGCAGA	OY 3301 TAGACAGCCATATCACAGATCCAGATCAAGAACAACGGCCTCTCCTAGAGCGGACCAC	Ay 3361 CACCGCTCCAGATCCTCTGAACCTCGATACAAACCTCATGAGGTCGATGACCTTCATT	OY 3421 AATGACTGCGCCCCCCCTCCTTCACCTGCCTTATCGAGGTCTCACCTCGTACGGG	DD 3481 GTCTGTCCAGACAACCCATCAAGTACTCCGGGAACAGGACGAAGGGGCCGACAACAAGCTTCC 3481 GTCTGTCCAGACAAGCCCATCAAGTACTCCGGGAAACAGGACGAGGAGCCTTCC	CY 3541 ACAGCTTCCACCAAAGGGAACATTGGAGAAGTGCTATGGATATTGGAGAGAAAATGG	OY 3601 CCAAATGAAACTTAACAAATACAAACAGTAGCCGGATCAGACCCCGGACTAGGAACAAGAAGAACAAATACAAACAGTAGCCCGAATCAGACCCCGAATGAACAAATACAAACAGTAGCCCGAATCAGACCCCGAATGAACAAATACAAATACAAATACAAATACAAACAGATAGAACCCCAAACCACCAAACAACAACAAATACAAACAA	OY 3661 TTACCATTCGAAGTATCGCTCAGGATCCACATAGAGGGGCAGATACTGTTTCC	Db 3661 TIACCATTCGAAGTATCGCTCAGGAATCGACATAGAGGGGCAGATACTGTTTCCAC
1561 GCGAGAAAAATGGAAACCATGTTAAGGAATGATTCTTTGAGTTCAGACCAGTCCGAGTC 1620 1621 AGTGAGGCCGCCCCCACCAAGGCCTCATAAATCCAAGAAAGGGGTAAAATGCGCCAGGT 1680 1621 AGTGAGGCCGCCCCCAAGGCCTCATAAATCCAAGAAAAGGAGGTAAAATCGACCAAGGT 1680	1681 TTCACTGAGGCGCGAGGAGGAGCTGGCATCCACACCTGAGTATACAAGCTGTGATGA 1740	AGANA	1801 AACTAGTGAGCAGGAGTTTTTGTCGGATTCTAACACCAGGTCTGAGAGACAAAAGAAAG		1921 GGACTCTGGGGGTAGATACCTGTAGTAGCACCATAACCGTAGCGTAGTGA 1980			AAAGT	AAAAAAAAAACTITIACTIGITACTIGIAGACAITCTIAGACCAGGIGAIGAAGTITIGGA	Angaranggargetartigearggagegecattitgaggargettacargattartietaga 	CHAP CHAP CHAP CHAP CHAP CHAP CHAP CHAP	8=8 8=8			0000		581 GAATICCITATGITTAGGATTTAGTTCCAGATAGAAGAAAAAAAAAA

Db 4861 CAGGTGGAAGCCCCTGGTAACACTGCTTGATGTTGTGTCTACAGAGCCCACGTCTA 4920 Qy 4921 GGGATACCAAGCAGTCCTGTGTTCTCAGAGAGAGTCGTAACATTGTGCCCTAGCAAGG 4980 Db 4921 GGGATACCAAGCAGTCTTCTCAGAGAAGTCGTACATTGTGCCCTAGCAAAGG 4980	RESULT 2 AAV40485 ID AAV40485 standard; CDNA; 1302 BP. XX XX AC AAV40485; AC AAV40485;	Human secreted protes. Secreted protein; CC Homo sapiens.	FH Key Location/Qualifiers FT CDS 1231247 FT XX FN W09831802-A1. XX XX XX XX XX XX XX XX XX XX XX XX XX	PF 21-JAN-1998; 98WO-US01007. RX		XX XX F-rough managero. XX X PT New isolated polymucleotides and secreted proteins - obtained from PT human foetal kidney, adult testes, placenta, adult brain and foetal PT brain cDNA libraries X XX XX Claim 22; Page 71-72; 104mm; English	XX XX XX XX XX XX County 1	•	CC activity, cycokine and cell proliteration/differentiation activity, communostimulant or immunosuppressive activity, heematopoiesis CC regulating activity, tissue growth activity, activity initialism cC activity, chemotactic or chemokinetic activity, hemotatic or thrombolytic activity, receptor/ligand activity, antiinflammatory CC activity, cadherin or tumour invasion suppressor activity, tumour cC inhibition activity, or other activities. XX Squence 1302 BP; 404 A; 286 C; 322 G; 286 T; 4 other;
3781 TCGTTTCAGCAGCACAAGCTACATGTCCGTCCAATCAGAGCGAGAGGAAACAGGAA 3840	3901 GACCAAAAGCACCAGCATCAGTGGAGACATGTGCTCACTGGAGAAGAATGACGGCAGCCA 3960	GGCCAAATGGTAGCTATTGTTGGTCCTCTCACGGAAAGTCGCAGTGCCTCTCAACTCGGAGTGCCTCTCAACTCGCAAAATGGTAGCTATTGTTGGTCTCTCTC	4081 CCAAACCGAAGGAGGAGATAAAAGCTACGAGCCACTGTTCAGAGAAGCACGAGACCGG 4140 4141 GCTAGCAGTGGAAGAAACTGGAATGACCGCCAGCCCGGGAATCCACAATGG 4200 4141 GCTAGCAGTGGAATGAGGAACTGGATGACCGCCAGGCCAGCCGGGAATCCACAGATGG 4200 4201 CAGCATGAACAGATGAGAAACTGGAATGACCGCCAGGCCAGGCCAGGCCGCGGGAATCCACAGATGG 4200 4201 CAGCATGAACAGCTATAAGAAGAAACTGGAAATCTTCCCTGGGGTCCCCCGCTGGCCTC 4260	4201 CAGCATGAACAGCTATAGCTCGGAAGGAAATCTGATCTTCCCTGGGGTCGGCCTGGGCTC 4260 4261 TGACAGCCAGTTCAGTGATTTCCTGGATGGCCTGGGCCTGGTCAGCTAGTGGGACCCC 4320	4321 GACCCTGGCTACTCCTGCAATGGGTGACATTCAGGTGGGAATGATGGATAAAAAGGGACA 4380 4321 GACCCTGGCTACTCCTGCAATGGGTGACATTCAGGTGGGAATGATGGATAAAAAGGGACA 4380 4381 GCTGGAGGTAGAAATCATCCGGGCGCGCGCCTTGTGGTAAAAACAGGACT 4440 4381 GCTGGAGGTAGAAATCATCCGGGCGCGCGCCTTGTGGTAAAACCAGGTTCCAAGACAT 4440	GCCAGCACCGTATGTCAAGGTGTATCTGTTAGACAACGGAGTCTGCATAGCCAAAAAGAA GCCAGCACCGTATGTCAAGGTGTATCTGTTAGACAACGGAGTCTGCATAGCCAAAAAGAA GCCAGCACCGTATGTCAAGGTGTATCTGTTAGACAACGGAGTCTGCATAGCCAAAAAGAA AACCAAGGTGGCGAGAAAGACCCTGGAGCCCCTGTAACGAACAGAAGAA		4621 CAATCCTTATGGGAGTGGCCCAGATACTCTAGATGAACTGGAACTATCCAACATGGT 4680 4621 CAAATCCTTATGGGAGTGGCCCAGATACTCTTAGATGAACTGGAACTATCCAACATGGT 4680 4681 GATTGGATGGTTCAAACTCTTCCCTCCTCCCTAGTAGATCCAACCTCGGCACCTCT 4740 4681 GATTGGATGGTTCAAACTCTTCCCTCCTTCCTCCCTAGTAGATCCAACCTCGGCACCTCT 4740 4681 GATTGGATGGTTCAAACTCTTCCCTCCTTCCTCCCCTAGTAGATCCAACCTCGGCACCTCT 4740	4741 GACAAGAAGAGCTTCCCAATCGTCTCTGGAAAGTTCTACCGGACCTTCTTACTCTCGTTC 4800 4741 GACAAGAAGAGCTTCCCAATCGTCTCTGGAAAGTTCTACCGGACCTTCTTACTCTGTTC 4800 4801 ATAGCAACTATAAAAACTGTTGTCACAACAACCAGAAAAACCAGAAAAAAACAA 4860 4801 ATAGCAACTATAAAAACTGTTGTCACAACAACCAGAAAAAACCAGAAAAAAAA

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1021 TITIACAGNICATCGICIGGGGAGATIATGGCCGCAIGGATCAATCTATTATGGGAG 1080
                                                                           4638 TOGCCCAGATACTCTTAGATGAACTGGAACTATCCAACATGGTGATTGGATGGTTCAAAC 4697
                                                                                                   1081 TOGCCCAGATACTTTAGATGAACTAGAGCTATCCAATATGGTGATCGGATGGTTCAAAC 1140
                                                                                                                                                                                     1141 TITICCACCITCCTCCCTAGTAGATCCAACCITGGCCCCTCTGACAAGAGAGTTCCC 1200
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to nucleic acids (AA198058-AA198161) or their homologues expressed by human neuroblastomas useful for detecting genes expressed by neuroblastoma and for analysing their structure and function. The nucleic acids are useful for the diagnosis and prognosis of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CCTCCTCCGCAGCCCGAGATGCCGGACCTCACCGCAACCACGGAGGAGAAAATC 148
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                                                                                                                                                          TCTTCCCTCCTTCCTCCCTAGTAGATCCAACCTCGGCACCTCTGACAAGAAGAGCTTCCC
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14.4%; Score 715; DB 22; Length 6637;
Best Local Similarity 57.2%; Pred. No. 1.28-194;
Matches 1771; Conservative 0; Mismatches 1045; Indels 279; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nucleic acids for prognosis of human neuroblastoma comprise nucleic acids expressed by human neuroblastomas -
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 6637 BP; 2020 A; 1423 C; 1511 G; 1683 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human neuroblastoma expressed polymucleotide SEQ ID NO 40.
                                                                                                                                                                                                                                                                                                                                                      1261 ATTGTTGTCACAGCAACCAGCGTTACABAAAAAAAAAA 1302
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12-MAY-2000; 2000JP-0140387.
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                                                                                                                  1 CAGGATGGGATCCTCATAGAGGGCAGATAATGTTTCTACTAAATCTTCGGACAGTGATG 60
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                                                       Gaps
        Score 844.8; DB 19; Length 1302;
Pred. No. 1.4e-232;
3; Mismatches 115; Indels 126;
           17.0%;
                                              Matches 1058; Conservative
Query Match
Best Local Similarity
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426 ATCATGGCAGTGATCGGCAGAAGGAAGGAGGAGAAAAAGAAGGAGCCATGCTCAAG 485 209 ATCAAAGAAAGAAAGCACAACCGACAGGGGGTTTCCCTTTAGTGGGATCACTGAA 268 486 TGTCTTGTCAGGGAATGGCAATGGCAAAGC	CTGGTAAATAAGTTCTGCGGCCCGGGAAAACGACCCAATGAGAAGGAGCCCCAGACACAAGAAAGTGCTGAAAAACGAGACCCAACAACCTTCACCAAGAT	AAGCTGCACCAATTTGAAATGTATAAGGAGCAAGTCAAGAAGATGGGGAGTTGGGAATCG 	389 CAGCAGCAGCAAGAGCAGAAGGTGATGCCCCGACCTGTGGCATCTGCCACAAGACA 445	446 AAAITIGGAGAIGGAGGCCARAAITGITCCIAITGCCAAACCAAGTICTGTGCTCGA 505	506 TGTGGAGGTCGAGTGTCTTTACGCTCAAACAAGGTTATGTGGGTGTGT 553	554 AAITHGIGCCGAAAACAACAAGAAATCCTCACTAAATCAGGAGCATGGTTTTATAAATAGT 613- 	614 GGGTCTAACACACTGCAGCAACCTGATCAAAAGGTTCCTCGAGGGCTTCGAAATGAG 670 	671 GAAGCCCTCAGGAGAAAGAAAACTACACGAGCGCCCCAGTTCCAAGAGCCCA 730 	731 GGTGACTTATCAGTACCTGCAGTTGAGAAGGCCGAGCTCATGGGCTCACAAGACAGGAT 790 987 AGCACAGCTGCCTCCTCCCAGGATGCTGCTCCTCCCCAGGGCTCCAGGAC 1040	791 ACTATTAAAATGGATCAGGAGTGAAGCACCAGATTGCCAGTGACATGCCTTCAGACAGA	851 AAACGAAGTCCATCAGGGATCAAAATCGAAGATACGAGGAAAGTGAAGAAAGA	911 GAGGACTACTCACAGTATGTTCCTTCAGATGCTACAATGCCAAGATCTCCTTCGGATTAT 970	971 GCTGATAGACGATCTCAGGGTGAGCCTCAATTTTATGAAGAACCTGGTCATTTAAATTAC 1030 1206 ACCTCAGGGGAGCCGTGGAGGGGGGGGGGGGGGGGGGGG	1031 AGGGATTCTAACAGGAGGCCATAGACATTCCAAAGAGTATATTGTGGATGATGAGGT 1090	1091 GTGGAGAGAGATGAATATGAAAGACAAAGGAGAGAGGAATACCAGGCAGG	1151 AGAAGTGATCCAAATCTGGCCGGTATCCCGTAAAGCCACAACCCTACGAAGAACAAATG 1210	1211 CGCATCCACGCTGACGGCACGACATGAGAGAAGGCACAGAGATGTTTTTTG 1270

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Composition useful for diagnosis of conditions, disorders or diseases associated with atherosclerosis, comprises several polymucleotides that are differentially expressed in foam cell development
                                                                                                                                                                                                                                                                                                                                                                                                                                               Mikita T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          641 Arcardádocrida crica de adade cada cada contra contra de de contra de de de contra de de contra de de contra de de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra 
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8.0%; Score 398.2; DB 24; Length 7325;
Best Local Similarity 67.9%; Pred. No. 3.4e-103;
Matches 556; Conservative 0; Mismatches 263; Indels: 0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                           Shiffman D, Somogyi R, Lawn R, Seilhamer JJ, Porter GJ,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; Page 123-125; 315pp; English.
                                                                                                                                                                                                                                         05-APR-2000; 2000US-195106P.
                                                                                                                                               04-APR-2001; 2001WO-US11128
                                                                                                                                                                                                                                                                                                                                       (INCY-) INCYTE GENOMICS INC
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1121 AAGACCTGTGATCCCCTGTACCAGCGCTCTGCTCTTTGACGAGGGACCCCCAGGGCAAG 1180
                                                                                                                GTGCTGCAGGTGATCGTCTGGGGAGACTATGGCCGCATGGACCACACAGAGTGCTTCATGGGC 1240
                                                                                                                                        4637 GTGGCCCAGATACTCTTAGATGAACTGGAACTATCCAACATGGTGATTGGATGGTTCAAA 4696
                                                                                                                                                        1241 ATGGCCCAGATCATGCTGGACGAGCTGGACCTCAGCGCCGCGGGTCACCGGCTGGTACAAA 1300
                                                                                                                                                                                        CTCTTCCCTCCTTCCTCCCTAGTAGATCCAACCTCGGCACCTCTGACAAGAAGAGCTTCC 4756
                                                                                                                                                                                                                 1301 CTCTTCCCCACCTCCTCAGTGGCAGACTCCACACTCGGATCCCTCAGGCGCGCTGTCC 1360
                                                                                       GTGTTACAGATCATTGTCTGGGGAGATTATGGTCGTATGGATCACAAATCCTTTATGGGA
                                                                                                                                                                                                                                                                                                                                                                                                                              Human, secreted protein, diagnosis, cytostatic, immunosuppressive; noctropic, neuroprotective, antiviral; antiallergic, hepatotropic, antidiabetic, antimilammatory, antiuloer; vulnerary, anticonvulsant, antibacterial; antifungal; antiparasitic, cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder; wound healing; neurological disease; infectious disease; chromosome identification;
                                                                                                                                                                                                                                         4757 CAATCGTCTCTGGAAAGTTCTACCGGACCTTCTTACTCT 4795
                                                                                                                                                                                                                                                                  1361 chgrerreceredadagadereceaececereargerer 1399
                                                                                                                                                                                                                                                                                                                                                                                                         Human secreted protein gene 46 SEQ ID NO:56.
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17-DEC-1999;
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Fifty nucleic acid molecules encoding human secreted proteins, useful in the prevention, treatment and diagnosis of cancer, immune disorders, cardiovascular disorders and neurological diseases -
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                                                                  Komatsoulis
(HUMA-) HUMAN GENOME SCI INC
                                                              Rosen CA, Ruben SM,
                                                                                                                             2000-594639/56.
                                                                                                                                                           P-PSDB; AAB34818.
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The polynucleotide sequences given in AAC59966 to AAC60015 encode the human secreted proteins given in AAB34773 to AAB34822. AAB34822 tepresent human secreted polypeptide sequences and proteins homologous to them, which are given in the exemplification of the present invention. Human secreted proteins have activities based on the tissues and cells the genes are expressed in. Examples of activities include: cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral;

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antiallergic; hepatotropic; antidiabetic; antiinflammatory; antiulcer; vulnerary; anticonvulsant; antidiabetic; antifungal; antiparasitic; and cardiant. The polymuclecides and polypeptides are useful for cardiant. The polymuclecides and polypeptides are useful for preventing, treating or ameliorating a medical condition in e.g. humans, mice, rabbits, goats, horses, cats, dogs, chickens or sheep. The polypeptides can also be used as a food additive or preservative to increase or decrease storage capabilities. The polymuclecides are useful for chromosome identification. They are also useful as probes for diagnosing a disorder related to the female reproductive system, or particularly breast and/or ovary cancer. They are also useful in the gene therapy of breast and ovarian cancer. Wucleic acids, protein, antibodies, agonists and antagonists from the present invention are useful in the diagnosis, treatment and prevention of cancer, immune disorders, cardiovascular disorders, wound healing, neurological diseases and in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4219
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4580 TTACAGATCATTGTCTGGGGAGATTATGGTGTATGGATCACAAATCCTTTATGGGAGTG 4639
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           96 AAAAAGTTAAAAAGTACCATCCAGAGAAGCACAGAAACAGGCATGGCAGCTGAAATGAGA 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATGGGTGATATACAAATAGGAATGGAGGACAAAAAAGGCCCAATTAGAAGTGGAAGTCATT 392
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29-SEP-2000;
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     Human; nootropic; neuroprotective; cytostatic; dermatological; virucide; immunosuppressive; antiinflammatory; anti-HIV; antibacterial; vulnerary; antiparkinsonian; antialsickling; antianaemic; antiarthritic; cancer; antirhemmatic; hepatotropic; cerebroprotective; antiinflammatory; antiallergic; antidiabetic; antiulcer; anticory; antidiabetic; antiulcer; anticory, antidiabetic; antiulcer; anticory, antidiabetic; antiulcer; anticory, antidiaparasitic; cardiant; immune disorder; cardiovascular disorder; neurological disease; infection; nephrotropic; gene therapy; vaccine; ss.
                                                                                                                  nervous system related polynucleotide SEQ ID NO 422.
                    ABA11415 standard; cDNA; 526 BP
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2000US-0220964.
2000US-0224518.
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16-MAR-2000;
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19-MAY-2000;
07-JUN-2000;
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01-SEP-2000;
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18-AUG-2000;
22-AUG-2000;
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3844 CAGTGTCTTTACATCCAAAATGCAAAACAGACAGATGGGCGTGTCGGGGAAGAACTTGAC 3903
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                                                                                                                                                                                                                                                                                                                                                                       Human; secreted protein; expressed sequence tag; BST; haematopolesis; tissue growth; activin; inhibin; chemotaxis; chemokinesis; haemostatic; receptor; ligand; thrombolytic; anti-inflammatory; cadherin; anti-tumour;
3531 GACAGCTTCCACACCTTCCACCAAAGGCAACATTGGAGAAAAAGGCTATGGATATAGA 3588
                                              301 GACAGCTTCCACCACACCAAAGGGAACGTTGGATAGAAAAGCAGGAGGTAAAAA 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present sequence represents a human expressed sequence tag (EST). The polymucleotide, which is a secreted EST, and the encoded protein are predicted to have useful biological activities which would make them suitable for treating, preventing or ameliorating medical conditions in humans and animals, although no supporting data is given. Suggested activities include nutritional activity, immune actimilating or suppressing activity, hammacocatic/chemokinetic activity, activin/inhibin activity, chemokinetic activity, hammostatic and thrombolytic activity, receptor/ligand activity, hammostatic and thrombolytic activity, receptor/ligand activity, anti-inflammatory activity, cadherin/tumour invasion suppressor activity, tumour inhibition activity, activity, the polymucleotide may also be useful for gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New polynucleotides encoding human secreted proteins - derived from e.g. human blood, kidney, foetal lung, placenta, testes, brain, ovary, pituitary, retina and colon cDNA libraries.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4.2%; Score 207.6; DB 20; Length 355; 90.2%; Pred. No. 5.1e-49; tive 0; Mismatches 24; Indels 0;
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Treacy M;
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                                                                                                                                                                        AAV90372 standard; cDNA; 355
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Agostino MJ, Jacobs K,
Racie LA, Spaulding V,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1999-070077/06.
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                                                                                                                                                                                                                                                                                                                      RST clone DM118.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3291 AAGCAGCAGATAGACAGCCATATCACAGATCCAGATCAACAGAACAACAGCCCTCTCCTAG 3350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 AAGCAGCAGATAGACAGCCATATCACAGATCCAGATCAACAGAACAACGGCCTCTCCTTG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CTCGTACTGGGGTCTGTCCAGACAAGCCCATCAAGTACTCCAGTCGCAGGACGAAGGGGCC 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to novel genes (ABAll004-ABA21534) and proteins (ABB14678-ABB18001) useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The mucleic acids, proteins, antibodies and (ant) agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune disorders e.g. Addison's disease, allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crobn's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c) cardiovascular disorders such as myocardial isolaemias; (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f) infections diseases such as viral, bacterial, fungal and parastici riffections.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nucleic acids encoding 3224 human nervous system antigen polypeptides, useful for preventing, diagnosing and/or treating nervous system
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 AGCGGACCACCACCCGCTCCAGATCCACTGAACGTCCTGATACAARCCTCATGAGGTCGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TGCCTTCATTAATGACTGGAAGATCTGCCCCTCCTTCACCTGCCTTATCGAGGTCTCACC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; SEQ ID NO 422; 1701pp + Sequence Listing; English
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2000US-0251989.
2000US-0251990.
                                                                                                                                                                                                                                                                                                                                                                       (HUMA-) HUMAN GENOME SCI INC
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                                                                                                                                                                                                                                                                                                                    05-JAN-2001; 2001US-0259678.
                                              2000US-0251160
                                                                   2000US-0251030,
2000US-0251988
                                                                                                                    2000US-0256719.
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                       2000US-0250391
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  useful for preventing, dicancers and metastases -
                                                                                                                                                                                                                                                                                                                                                                                                                      Rosen CA, Barash SC,
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P-PSDB; ABB15089.
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                                                                05-DEC-2000;
05-DEC-2000;
05-DEC-2000;
06-DEC-2000;
08-DEC-2000;
08-DEC-2000;
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3844 CAGTGTCTTTACATCCAAAATGCAAAACAGACAGATGGGCGTGTCGGGGAAGAACTTGAC 3903

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Human; open reading frame; ORFX; detection; cytostatic; hepatotropic; vulnerary; antipeoriatic; antiparkinsonian; nootropic; neuroprotective; anticorvulsant; osteopathic; antiarthritic; immunostimulant; thrombolytic; cosquiant; vasotropic; antidabetic; immunostimulant; thrombolytic; cosquiant; vasotropic; antidabetic; hypotensive; dermatological; immunosuppressive; antilinflammatory; antitival; antibacterial; antifungal; antitirheumatic; antiliry antidabetic; antidabetic; antidabetic; antidabetic; antidabetic; antidabetic; antidabetic; antidabetic; proliferative disorder; hypotrension; neurodegenerative disorder; osteoarthritis; graft vs host disease; cardiovascular disease; diabetes mellitus; hypothroidism; SCID; AIDS; cholesterol ester storage; systemic lupus erythematosus; infection; sebma; severe combined immunodeficiency; malaria; autoimmune disorder; asthma; allergy; aplastic anaemia; nocturnal haemoglobinuria; bun; wound; bone damage; cartilage damage; antiinflammatory disease; coaqulation; uttrombosis; contraceptive; ss.
                                                               4024 CABARGGTAGTTGTTGGTCTCTCACGGAAAGTCGCAGTGCTCTCAACTCAGCCA 4083
169 AAAAAGCACCAGCATCAGTQAQAACATGTQCTCACTGAAAAAAAATGATGGCAGCCAGTC 228
                                                                                          229 TORCHCHOCHOTGGGCACCTTGGGCACCAGTGGCAAAAAGCGGCGCTCTAGCCTTGGTGC 288
                                                                                                                                                                    289 CARANTOGIAGCIAICGITGGICGICAGGAAAAGICGCAGIGCIICICAGGGGG 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAC7446 to AAC77606 encode the proteins given in AAB40237 to AAB43397, which represent the human ORFX open reading frames 1 to 3161. The ORFX sequences have activities such as: cytostatic; hepatotropic; vulnerary; antipsoriatic; antiparkinsonian; noortopic; neuroprotective; osteopathic; anticonvulsant; antiatchritic; immunosuppressant; immunostimulant; cardiant; thrombolytic; coagulant; vasotropic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel nucleic acids and peptides derived from open reading useful for treating e.g. cancers, proliferative disorders, neurodegenerative disorders and cardiovascular disease -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human ORFX ORF489 polynucleotide sequence SEQ ID NO:977.
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                                                                                                                                                                                                                                                                                                                                                                    AAC74934 standard; cDNA; 378 BP.
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02-APR-1999; 99US-0127636.
05-APR-1999; 99US-0127728.
30-MAR-2000; 2000US-0540763.
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P-PSDB; AAB40725.
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11-JUL-2000; 2000US-0614150.

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                         antinflammatory; antibacterial; antifungal; antifungal; antifundatio; antifungal; antibacterial; antifungal; antifungal; antifundatio; antifungal; antifungal; antifungal; antifungal; antifungal; antifungal; antifungal; antifungal; antifungal; antifungal; antifungal; antifungal; antifungal; and antifungal; antifungal; and antifungal; and antifungal; and any be used to treat cancers, proliferative disorders, neurodegenerative disorders, osteoarthritis, proliferative disorders, cardiovascular disease, disbetes mellitus, hypertension, hypothyroidism, cholesterol ester storage, systemic lupus erythematosus, severe combined immunodeficiency (SCID), AIDS, viral, allergies, aplastic anesmia, burns, wounds, borne and cartilage damage, nocturnal haemoglobinuria, antiinflammatory disease; to enhance coagulation; to inhibit thrombosis; and as a contraceptive.
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antidiabetic; hypotensive; dermatological; immunosuppressive;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 3.9%; Score 195.6; DB 21; Length Best Local Similarity 71.3%; Pred. No. 1.5e-45; Matches 258; Conservative 0; Mismatches 104; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 378 BP; 85 A; 106 C; 130 G; 57 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABL12715 standard; cDNA; 7395 BP.
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                                                                                                                                                                                                                                                                     The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactional higher enkaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16175-ABL30511), expressed DNA sequences (ABL16175) and the encoded proteins
(ABBS7737-ABB72072).

The sequence data for this patent did nelectronic format of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
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                                                                                                                                                              New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7115 CTCGACGCACCCTGGATCCACTGTATCAGCAGCTTGGTATTCAAGCAGTCCTACACCG
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                                                                                                                                                                                                                                          Claim 1; SEQ ID NO 32627; 21pp + Sequence Listing; English.
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                                                                       Myers EW
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                                                                     Venter JC, Adams M,
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Human; foetal liver; gene expression; single exon nucleic acid probe; ss.

30-JAN-2001; 2001#O-US00669

04-PEB-2000;

WO200157277-A2. Homo sapiens.

09-AUG-2001,

Human foetal liver single exon nucleic acid probe #4240.

01-FEB-2002

ABA55935;

341 TTAGTGCCAAGTGGTTGCCATAGT 365

a .

ABA55935 standard; DNA, 365 BP

RESULT 12

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The invention relates to a spatially-addressable set of single exon nucleic acid probes for measuring gene expression in a sample derived from human breast and BY 474 cells. The method involves contacting the probes with a collection of detectably labelled mucleic acids carried from mana of the microarray. The probes are useful for verifying the expression of regions of genomic DAA predicted to encode proteins. They are useful for gene discovery, and for encode proteins. They are useful for gene discovery, and for encode proteins. They are useful for sassassing the toxicity of chemical expression analysis is useful for assessing the toxicity of chemical agents on cells. The microarray of this invention presents a far greater diversity of probes for measuring gene expression, with far less bias conversity of probes for measuring gene expression, with far less bias can repid production of functional information from genence. The present sequence is a single exon nucleic acid probe of the invention. Note: The sequence data for this patent did not form part of the conversion of the invention. The matter of the invention of printed specification, but was obtained in electronic format directly conversions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    161 GTAAATATAGTTCATTTACCCCCAAAATGCAAGGCAGACGGAAGATTCAGGAAGAT 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New spatially-addressable set of single exon nucleic acid probes, useful for measuring gene expression in sample derived from human breast, comprises number of single exon nucleic acid probes -
                                                       Human; microarray; single exon probe; gene expression; breast;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2.3%; Score 113.8; DB 22; Length 365; 72.2%; Pred. No. 6.1e-22; Live 0; Mismatches 57; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; SEQ ID NO 4132; 327pp + sequence listing; English.
                 Human breast cell single exon nucleic acid probe #4132.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 365 BP; 111 A; 62 C; 90 G; 102 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chen W, Rank DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                    04-FEB-2000; 2000US-0180312.
26-MAY-2000; 2000US-0207456.
30-UIN-2000; 2000US-0608408.
03-AUG-2000; 2000US-0632366.
21-SEP-2000; 2000US-0234687.
27-SEP-2000; 2000US-0234597.
                                                                                                                                                                                                                                            30-JAN-2001; 2001WO-US00662.
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Matches 148; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Penn SG, Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-496933/54.
                                                                                  disease; cancer; ss
                                                                                                                                                               WO200157271-A2.
                                                                                                                         Homo sapiens.
                                                                                                                                                                                                       09-AUG-2001
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GCCAGTCCGACACTGCAGTGGGCGCCTGGGTACCAGTGGCAAAAACGGCGATCTAGCA 4016
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          161 GTAAATATAGTTCATTTACCCCAAAATGCAAGGCAGACGAAGATGGGAACTTCAGGAAGAT 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        221 CCATCATGAAGACACCAGTGACAGTGAGAGATGTACACACTGGAGCTATAATGACGGCA 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         281 GCCAGTCAGACAGCTGTGGGTACAGTTGGAGCAGGTGGAAAAGAAAAGAAAATGCAGCC 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to a single exon mucleic acid probe for measuring human gene expression in a sample derived from human foetal liver. The single exon mucleic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from human fetal liver. The present sequence is a single exon nucleic acid probe of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human fetal liver
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2.3%; Score 113.8; DB 22; Length 365;
Best Local Similarity 72.2%; Pred. No. 6.1e-22;
Matches 148; Conservative 0; Mismatches 57; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; SEQ ID NO 4240; 639pp + sequence listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 365 BP; 111 A; 62 C; 90 G; 102 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Penn 8G, Hanzel DK, Chen W, Rank DR;
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30-UNN-2000; 2000US-0608408.
03-AUG-2000; 2000US-0633366.
21-SEP-2000; 2000US-0234687.
27-SEP-2000; 2000US-023459.
04-OCT-2000; 2000GB-0024263.
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221 CCATCATGAAGAGCACCAGTGTGGAGGATGTACACACTGGAGCATAATGACGGCA

GCCAGTCCGACACTGCAGTGGGCGCCCTGGGTACCAGTGGCLAAGAAGCGGCGATCTAGCA 4016

3957

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TTGGGGCCAAATGGTAGCTATTGT 4041

4017

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3897 ACTITGACCAAAAGCACCAGCATCAGTGGAGACATGTGCTCACTGGAGAAGGAATGACGGCA 3956
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention relates to single exon nucleic acid probes for measuring human gene expression in a sample derived from human heart. The present sequence is one such probes may be used for predicting, measuring and displaying gene expression in samples derived from the human heart via microarrays. By measuring gene expression, the probes are useful for predicting, diagnosting, grading, staging, monitoring and prognosing diseases of the human heart and vascular system expression and prognosing diseases of the human heart and vascular system expression and prognosing diseases.
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Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Single exon nucleic acid probes for analyzing gene expression in human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                         Probe #4068 for gene expression analysis in human heart cell sample.
                                                                                                                                                                        gene expression, heart; microarray; vascular system; probe; vascular disease; hypertension; cardiac arrhythmia;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 365 BP; 111 A; 62 C; 90 G; 102 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chen W, Rank DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (MOLE-) MOLECULAR DYNAMICS INC.
                                 ABA25602 standard; DNA; 365 BP
                                                                                                                                                                                                                                                                                                                                                                                                         26-MAY-2000; 2000US-0207456.
30-JUN-2000; 2000US-0608408.
03-AUG-2000; 2000US-0632366.
21-SEP-2000; 2000US-0234687.
27-SEP-2000; 2000US-0234687.
04-OCT-2000; 2000GB-0024263.
                                                                                                                                                                                                               congenital heart disease; ss
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                                                                                                      (first entry)
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                                                                                                                                                                                                                                                                                WO200157274-A2
                                                                                                                                                                                                                                                   Homo sapiens.
                                                                                                      23-JAN-2002
                                                                                                                                                                                                                                                                                                                      09-AUG-2001.
                                                                    ABA25602;
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                                                                                                                                                                          Human;
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GCCAGTCCGACACTGCAGTGGGCGCCTGGGTACCAGTGGCAACAAGAGCGGCGATCTAGCA 4016
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 161 GTAAATATAGITCATITACCCCCAAAATGCAAGGCAGACGACGATGGGGACTTCAGGAAGAT 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human broain. They can be used to measure gene expression in brain cell samples, which may enable the diagnosis and improved treatment of nervous system diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia, epilepsy and cancers. The present sequence is one of the probes of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Single exon nucleic acid probes for analyzing gene expression in human
                                                                                                                                                                                                                        Human; brain expressed exon; gene expression analysis; probe; microarray; Alzheimer's disease; multiple sclerosis; schizophrenia;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 4; SEQ ID NO: 4139; 650pp + Sequence Listing; English.
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                                                                                                                                                                                          Human brain expressed single exon probe SEQ ID NO: 4139
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4017 TTGGGGCCAAAATGGTAGCTATTGT 4041
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                            341 macreccaalgrecineccanaci 365
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                                                                                                     AAK04148 standard; DNA; 365
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                                                                                                                                                                                                                                                                                                                                                                                                                                                03-AUG-2000; 2000US-0632366.
21-SEP-2000; 2000US-0234687.
27-SEP-2000; 2000US-0236359.
04-OCI-2000; 2000GB-0024263.
                                                                                                                                                                                                                                                                                                                                                                                                                                  2000US-0608408
                                                                                                                                                              (first entry)
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                                                                                                                                                                                                                                                       epilepsy; cancer; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2001-483446/52.
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                                                                                                                                                                                                                                                                                                               WO200157275-A2.
                                                                                                                                                                                                                                                                                   Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                      04-FBB-2000;
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3897 ACTIGACCAAAAGCACCAGCAICAGIGGAGACAIGIGCICCACIGGAGAAGAAIGACGACA 3956
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human bone marrow. They can be used to measure gene expression in bone marrow samples, which may enable the improved diagnosis and treatment of cancers such as lymphoma, leukable the improved diagnosis and treatment of cancers the probes of the invention.
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                                                                                                                                                                                                                               Human; bone marrow expressed exon; gene expression analysis; probe; microarray; cancer; leukaemia; lymphoma; myeloma; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human bone marrow -
                                                                                                                                                                                                 Human bone marrow expressed single exon probe SEQ ID NO: 4187.
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4017 TTGGGGCCAAAATGGTAGCTATTGT 4041
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                341 TTAGTGCCAAAGTGGTTGCCATAGT 365
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                                                                                                        AAK29630 standard; DNA; 365 BP
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21-SEP-2000; 2000US-0234687.
27-SEP-2000; 2000US-0236359.
04-OCT-2000; 2000GB-0024263.
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                                                                                                                                                                06-NOV-2001 (first entry)
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30-JUN-2000;
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Search completed: December 11, 2003, 15:51:13 Job time : 1181 secs

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Sequence 14, Appl Sequence 24, Appl Patent No. 5482709 Sequence 1, Appli Sequence 1, Appli Sequence 20, Appl Sequence 20, Appl Sequence 2, Appl Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 16, Appli Sequence 16, Appli Sequence 16, Appli Sequence 16, Appli Sequence 16, Appli Sequence 16, Appli Sequence 18, Appli Sequence 18, Appli Sequence 18, Appli Sequence 11, Appli Sequence 17, Appli
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Sequence 7, Appli
Sequence 159, App
Sequence 209, App
Sequence 3332, Ap
Sequence 7, Appli
Sequence 2, Appli
Sequence 1, Appli
                                                                                                   December 11, 2003, 15:31:19 ; Search time 306 Seconds (without alignments) 7183.294 Million cell updates/sec
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/cgn2_6/ptcdata/2/ina/PcTUS_COMB.seq:*
/cgn2_6/ptcdata/2/ina/PcTUS_COMB.seq:*
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-09-094-714A-48
US-09-094-714A-48
US-09-25-749-24
US-08-72-749-24
US-08-72-689-10
US-09-210-399-10
US-09-10-399-10
US-09-10-585-1
US-09-10-585-1
US-09-10-585-1
US-09-10-551B-10
US-09-410-551B-10
S-09-411-350-77
US-09-328-352-3332
US-09-411-350-77
US-09-328-352-3332
US-09-411-350-77
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                                                                                                                                                                                                                                                                                                    569978 Beqs, 220691566 residues
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                                                                                                                                                                                                                                                                                                                                                                                                                            Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                     OM nucleic - nucleic search, using sw model
                                                                                                                                                                                                                                                                   Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Patents_NA:*
                                                                                                                                                                                                                                                                                                                                                                        Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                             US-09-617-099B-2
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Match Length
                                                                                                                                                                                                                                                 IDENTITY NUC
                                                                                                                                                                                             Perfect score:
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                                                                                                                                                                                                               Sequence:
                                                                                                                                                                                                                                                                                                    Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Database
                                                                                                          Run on:
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543 6 5273901-6 542 3 08-09-084-843A 542 3 08-09-016-315- 542 4 08-09-018-18- 553 4 08-09-203-895- 554 4 08-09-203-895- 554 4 08-09-203-895- 554 1 08-08-257-803B 555 2 08-08-628- 556 2 08-08-628- 557 2 08-08-628- 558 2 08-08-628- 558 2 08-08-68- 558 2 08-68- 568 2 08- 568 06		63-14/c 14, Application US/08232463 5, 5670367	(X	SCHILLINGER, F.	RECOMBINANT FOWLPOX VIRUS	DDRKSS: ley & Lardner Diagonal Road, Smite Ann			R FORM: Floppy disk	atible DOS/MS-DOS Lease #1 0 Version #1	; s/08/232,463	435	R: US/07/935,313	APPLICATION NUMBER: EP 91 114 300.6 FILING DATE: 26-AUG-1991	RMATION: hen A. Pb. 30 769	H 2)))	OR SEQ ID NO: 14: ARRACTERISTICS: 7218 Base pairs	aciu single		
	00		cati	ATION:	SCHEIFLI FALKNER,	TON:	Foley	dria	299	FICE	M PC TEM:	TION	2 S	TOWER TO	UMBE 26-	INFC Step Mind	ON I	3) 68	TERI	Cac Bat Bear B:	t-P1
000000000000000000000000000000000000000			/c pp11	TAT	S S S	INVENTION:		Alexandria VA	X: USA 22313-0299	READAB TYPE:	SYSTE	IJ N	TE: ATIO	NE NE	Z Z		/bod/	(703) 899149	28 S	DNESS: TY: line SOURCE:	pTzgpt-F18
	39.6			NERAL INFORMATION: APPLICANT: DORNER	APPLICANT: APPLICANT:	TITLE OF INVENTION: NUMBER OF SEQUENCES	CORRESPONDENCE ADDRESS ADDRESSEE: Foley & STREET: 1800 Diagon	CITY: Alex	COUNTRY: ZIP: 223:	COMPUTER READABLE FORM: MEDIUM TYPE: Floppy	COMPUTER: IBM PC OPERATING SYSTEM: SOPTWARE: Patent	CURRENT APPLICATION DATA APPLICATION NUMBER: U	FILING DATE: CLASSIFICATION: 435 PRIOR APPLICATION DATE:	APPLICATION NUMBER: FILING DATE:	APPLICATION NUMBER: FILING DATE: 26-AU	TORNEY/AGENT INFORMA NAME: BENT, Stephen REGISTPATION WIMPED:	REFERENCE/DOCKET NUMBER: LECOMMUNICATION INFORMAT TRIEBHONE: (703) 836-930	TELEX: 89	INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS INFORMATION 17218 DASS PAI	7 19 15 12	
800048646666600444446666666666666666666	ι <u>α</u>	5	Sequence	GENERAL	Z Z	H E	3 ~ "	J W	J 14	8 ~		8	20 -	4		E ~ "	THE T	- 67 64	SES SES	. w. E	8-23
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DB 1; Length 7218;

1.3%; Score 67.2;

Query Match

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                                                                                                                                    1708 GGCATCCACACCTGAGTATACAAGCTGTGATGATGTGGAGGCTGGAAAGCGAGAGTGTGAG 1767
                                                                                                                                                                                                                 1768 TGAGAAAGGGGACAGTCAAAAGGGAAAAAAAAAACTAGTGAGCAGGGAGTTTTGTCGGA 1827
                                                                                                                                                                                                                                                                                            1828 ITCTAACACCCAGGTCTGAGAGACAAAAGAAAAGGATGTACTATGGTGGCCACTCTTTGGA 1887
                                                                                                                                                                                                                                                                                                                                                                                                                                                   1948 CACAACCTTAACGAGGAGCATAGCCATAGTGATAAGCACCCTGTGACCTGGCGAGCCATC 2007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2008 CAAAGATGGAGATCGCCTAATTGGTCGTATTTTATTAAATAAGCGTTTTAAAAGATGGGAG 2067
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:

APPLICANT: C. Frank Bennett, Nicholas M. Dean
APPLICANT: C. Frank Bennett, Nicholas M. Dean
TITLE OF INVENTION: OLIGONUCLEOTIDES FOR ENHANCED MODULATION OF
TITLE OF INVENTION: PROTEIN KINASE C EXPRESSION
NUMBER OF SEQUENCES: 69
CORRESPONDENCES: 69
CORRESPONDENCE ADDRESS:
ADDRESSER: Woodcock Washburn Kurtz Mackiewicz & No. 6117847ris, LLP
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
                      Gaps
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Best Local Similarity 6.4%; Fred. No. 3.8e-09; Matches 27; Conservative 232; Mismatches 165; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPR: DISKETTE, 3.5 INCH, 1.44 MD STORAGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: WORDPERFECT 8.0
CURRENT APPLICATION DATA:
RILING CATION NUMBER: US/09/094,714A
FILING DATE: June 15, 1998
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRICE ASSISTANCE AND STATE APPLICATION NUMBER: 08/601,269 FILING DATE: 14-FEB-1996 PRICE APPLICATION NUMBER: 08/478,178 FILING DATE: 07-JUN-1995 PRICE APPLICATION DATE: 08/089,996 FILING DATE: 09-JUL-1993 PRICE APPLICATION NUMBER: 08/089,996 FILING DATE: 09-JUL-1993 PRICE APPLICATION DATE: FILING DATE: 16-MAR-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 48, Application US/09094714A
Patent No. 6117847
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2068 TGTA 2071
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US-09-094-714A-48
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2489 ATAAAACTIATGGTTTGACAAGGTTGGTCACCAGTTGATAGTTACAATTTTTGGGAGCAAAG 2548
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APPLICANT: Dean, Nicholas M.
APPLICANT: Dean, Nicholas M.
APPLICANT: Dean, Nicholas M.
APPLICANT: McKay, Robert, A.
TITLE OF INVENTION: Modulation of c-jun using inhibitors of protein kinase (FILE REFERENCE: ISIS3313
CURRENT APPLICATION NUMBER: US/09/225,749
CURRENT FILING DATE: 1999-01-05
NUMBER OF SEQ ID NOS: 24
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 24
LENGTH: 2245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                511 ATTTACCTAAAGGCIGAGGTTGCTGAATGGTCCCATGTCACAGTACGAGATGCAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        571 AATCTAATCCCTATGGATCCAAACGGGCTTTCAGATCCTTATGTGAAGCTGAAACTTATT
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Pred. No. 0.0015;
0; Mismatches 139; Indels 0
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48.5%; Pred. No. 0.0015;
tive 0; Mismatches 139; Indels 0
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DATE: 1990-04-25
DATE: SP0-04-25
DATE: MARKER: X52479/Genbank
DATABASE RNTRY DATE: 1993-09-12
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         1.0%;
ITTORNEY/AGENT INFORMATION:
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NAME/KRY: CDS
LOCATION: (28)...(2046)
FUBLICATION INFORMATION:
JOURNAL: Rucleic Acids Res.
VOLUME: 18
                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 48.5<sup>3</sup>
Matches 131; Conservative
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Best Local Similarity 48.5
Matches 131; Conservative
                                                                                                                                                                                                                           ; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
UB-09-094-714A-48
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ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                       APPLICANT: Chang, Yuan
APPLICANT: Bohenzky, Roy A.
APPLICANT: Behenzky, Roy A.
APPLICANT: Bales J.
APPLICANT: Moore, James J.
APPLICANT: Moore, Patrick S.
TITLE OF INVENTION: Immediate Rarly Protein From Kaposi's
TITLE OF INVENTION: Sarcoma-Associated Herpesvirus, DNA
TITLE OF INVENTION: Barcoma-Associated HE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
0.9%; Score 45; DB 2; Length 3489;
Best Local Similarity 48.6%; Pred. No. 0.013;
Matches 123; Conservative 0; Mismatches 130; Indels
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
SOFTWARE: Patentin Release #1.0, Yersion #1.30
APPLICATION NUMBER: US/08/728,323A
FILING DATE:
                                                                                                                            Sequence 1, Application US/08728323A
Patent No. 5948676
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ATTORNEY/ASENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFRENCE/POCKEY NUMBER: 0575
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-278-0400
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MOLECULE TYPE: DNA (genomic)
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3489 base pairs
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STRANDEDNESS: sing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1..3489
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US-08-728-323A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY:
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                                                                                                                            2549 GAICTCCCTTCCAGGGAAGATGGAAGGCCAAGGAATCCTTATGTTAAGATTTACTTCCTT 2608
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511 ATTTACCTAAAGGCTGAGGTTGCTGAAAAGCTCCATGTCACAGTACGAGATGCAAAA 570
                                                                                                                                                                                                                                                         571 AATCTAATCCCTATGGATCCAAACGGGCTTTCAGATCCTTATGTGAAGCTGAAACTTATT 630
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TITLE OF INVENTION: EIMERIA ANTIGENIC COMPOSITION WHICH FILLITS ANTIBODIES AGAINST AVIAN COCCIDIOSIS
NUMBER OF SEQUENCES: 10
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 0.9%; Score 46; DB 6; Length 533; Best Local Similarity 49.0%; Pred. No. 0.0016; Matches 150; Conservative 0; Mismatches 155; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2729 CIGGAAATTACCCTTIGGGAICAAGCIAGA 2758
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FILING DATE: 08-NOV-1993
RELOR APPLICATION DATA:
APPLICATION NUMBER: 581,693
FILING DATE: 12-828-1990
APPLICATION NUMBER: 215,162
FILING DATE: 05-JUL-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: 746,520
FILING DATE: 19-JUN-1985
APPLICATION NUMBER: 627,811
FILING DATE: 05-JUL-1984
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2109 GGATGAGCAGCAGCAGGATGAGCAGGAGCAGCAGGATGAGCAGCAGCAGGATGAGCA
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                                                                                     289 GCCCCAGCAAAACAACCAATGAGAAGCACCCCAGACAAAGCTGCACCAACAATTTGA 348
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Chang, Yuan
APPLICANT: Russo, James J.
APPLICANT: Russo, James J.
APPLICANT: Russo, James J.
APPLICANT: Russo, James J.
APPLICANT: Russo, James J.
APPLICANT: Roce, Patrick S.
APPLICANT: Roce, Patrick S.
TITLE OF INVENTION: POLIVEPITIDES FROM KAPOSI'S SARCOMA-ASSOCIATED
TITLE OF INVENTION: HERESVIRUS, DNA ENCODING SAME AND USES THEREOF
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSER: COOPER & Dunham Lip
STREET: 1135 Avenue of the Americas
Best Local Similarity 48.6%; Pred. No. 0.013;
Matches 123; Conservative 0; Mismatches 130; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADPLICATION WUMBER: US/08/770,379
FILING DATE:
CLASSIPTCATION: 435
CLASSIPTCATION: 435
ATTOCNEY AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REGISTRATION NUMBER: 52342
REFERENCE/DOCKET NUMBER: 52342
TELEPHONE: (212) 278-0400
TELEPHONE: (212) 278-0400
TELEPHONE: (212) 391-0525
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 32207 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      U8-08-770-379-20/c
; Sequence 20, Application US/08770379
; Patent No. 5849564
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MOLECULE TYPE: DNA (genomic)
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TYPE: nucleic acid
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Best Local Similarity 48.6
Matches 123; Conservative
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STATE: New York
COUNTRY: U.S.A.
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Sequence 1, Application US/09410399

Patent No. 6482587

GENERAL INFORMATION:
APPLICANT: Cotter, Murray A.

TITLE OF INVENTION: Methods to Inhibit or Enhance the Binding of Viral DNA TITLE OF INVENTION: to Genomic Host DNA TITLE OF INVENTION: to Genomic Host DNA TITLE OF INVENTION: to Genomic Host DNA CURRENT APPLICATION NUMBER: US/09/410,399

CURRENT FILING DATE: 1999-10-01
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                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Kieff, Elliott D.
APPLICANT: Kieff, Elliott D.
APPLICANT: Mallestas, Mary R.
APPLICANT: Kaye, Kenneth M.
TITLE OF INVENTION: RHADINO VIRUS LANA ACTS IN TRANS ON A UNIT OF RHADINO
TITLE OF INVENTION: VIRUS DNA TO MEDIATE RFFICIENT RPISOME PERSISTENCE
FILE REFERENCE: 16412-10001R
CURRENT APPLICATION NUMBER: US/09/298,568
CURRENT FILING DATE: 1999-04-21
BARLIER APPLICATION NUMBER: US 60/109,422
BARLIER FILING DATE: 1999-11-19
NUMBER OF SEQ ID NOS: 3
SOFTWARE: PATENTIN VET: 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0.9%; Score 45; DB 4; Length 3489;
48.6%; Pred. No. 0.013;
tive 0; Mismatches 130; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; ORGANISM: Kaposi's sarcoma-associated herpesvirus
US-09-298-568-1
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                                                                                                                                                                        // Sequence 1, Application US/09298568
// Patent No. 6322792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2229 GCAGGATGAGCAG 2241
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SEQ ID NO 1
LENGTH: 3489
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Matches 123; Conservative
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0.9%; Score 45; DB 2; Length 32207;
48.6%; Pred. No. 0.065;
tive 0; Mismatches 130; Indels (
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APPLICANT: Chang, Yuan
APPLICANT: Ruseso, James J
APPLICANT: Ruseso, James J
APPLICANT: Ruseso, James J
APPLICANT: Ruseso, James J
APPLICANT: Ruseso, James J
APPLICANT: Bolnan, Isidore S
APPLICANT: Moore, Patrick S
TITLE OF INVENTION: UNIQUE ASSOCIATED KAPOSI'S SARCOMA VIRUS SEQUENCES AND
TITLE OF INVENTION: USES THENOF
FILE REFERENCE: 45185-G-PCT-US
CURRENT FILING DATE: 1999-11-17
FRIOR APPLICATION NUMBER: PCT/US97/13346
FRIOR FILING DATE: 1997-07-22
NUMBER OF SEQ ID NOS: 30
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 20
IENGTH: 32207
                                          19828 GCAĠCAGCAĠĠATGAĠCAGCAĠCAĠCAĠĠATĠAĠĊĊĠĊCAĠĊAĠĠAŢGAĠCAĠĊAĠCA 19769
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229 ACAACCGACACAGTGGTTTTCCCTTTAGTGGGATCACTGAACTGGTAAATAACGTTCTGCA 288
                                                                                            289 GCCCCAGCAAAAACAACCCAATGAGAAGGAGCCCCAGACAAAGCTGCACCAACAATTTGA 348
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48.6%; Pred. No. 0.065;
Live 0; Mismatches 130; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; TYPE: DNA; CAPOSI's BALCOMA-ASSOCIAted herpesvirus US-09-230-371A-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 20, Application US/09230371A Patent No. 6348586
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; Sequence 3, Application US/09181585
; Patent No. 6524791
; GRNERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                     19768 GCAGGATGAGCAG 19756
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Matches 123; Conservative
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               19888 GGATGAGCAGGAGCAGGATGAGCAGGAGCAGCAGGATGAGCAGCAGCATGAGCATGAGCA
                                                                                                                                                                                                                                                                                                       19828 GCAGCÁGCÁGCÁGCÁGCAGCÁGCAGGATGÁGCÁGCAGCÁGCÁGCÁGGÁTGÁGCÁGCÁ 19769
                                                                                                           19948 TGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGGATGAGCAGGAGCAGCA 19889
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                                                                                                                                                             289 GCCCCAGCAAAACAACCCAATGAGAAGGAGCCCCAGACAAAGCTGCACCAACAATTTGA 348
                                                                                                                                                                                                                                                          349 AATGTATAAGGAGCAAGTCAAGAAGATGGGAGAGGAATCGCAGCAGCAGCAAGAGCAGAA 408
                                                                 229 ACAACCGACACAGTGGTTTCCCTTTAGTGGGATCACTGAAACTGGTAAATAACGTTCTGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 169 TCAGAAGAAGAAGAAGAGAAGAAGAGCAGTCCGTGCTCAAGATCAAAGAAGAACAAAAGC
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APPLICANT: Chang, Yuan
APPLICANT: Russo, James J.
APPLICANT: Russo, James J.
APPLICANT: Releman, Isidore S.
APPLICANT: Releman, Isidore S.
TITLE OF INVENTION: UNIQUE ASSOCIATED KAPOSI'S SARCOMA VIRUS
TITLE OF INVENTION: SEQUENCES AND USES THEREOF
NUMBER OF SEQUENCES: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 45; DB 3; Length 32207;
Pred. No. 0.065;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches 130; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/757,669A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          : Cooper & Dunham LLP
1185 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 20, Application US/08757669A Patent No. 6183751
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/POCKET NUMBER: 4518
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: (212) 278-0400
TELEPAX: (212) 391-0525
INFORMATION FOR SEQ ID NO: 20: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; MOLECULE TYPE: DNA (genomic)
US-08-757-669A-20
                                                                                                                                                                                                                                                                                                                                                                                                    19768 GCAGGATGAGCAG 19756
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TYPE: nucleic acid
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U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: nucleic
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 9
US-08-757-669A-20/c
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243 GGITTCCCTTTAGTGGGATCACTGAACTGGTAAATAACGTTCTGCAGCCCCAGCAAAAC 302
                                                            Sequence 3, Application US/09253691
Patent No. 6124100
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// Patent No. 6524791
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                       RESULT 13
US-09-181-585-2/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             183 AGGAGAAGGAGCAGTCCGTGCTCAAGATCAAAGAAGAACACAAAGCAAAGCAACCGACACAGT 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            243 GGTTTCCCTTTAGTGGGATCACTGAACTGGTAAATAACGTTCTGCAGCCCCCAGCAAAAAC 302
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               123 ACCTCACGGAAGAGGAGGAAAATCATCCTGGCTGTCATGGATCGTCAGAAGAAGAAG 182
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APPLICANT: Koob, Michael
TITLE OF INVENTION: SPINOCERBELLAR ATAXIA TYPE 8 AND METHODS OF DETECTION
FILE SPEEKENCE: 110,0001001
CURRENT APPLICATION NUMBER: US/09/181,585
CURRENT FILING DATE: 1998-10-28
NUMBER OF SEQ ID NOS: 18
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 3
LENGTH: 1037
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: SPINOCEREBELLAR ATAXIA TYPE 8 AND METHODS OF DETECTION FILE REFERENCE: 11,00090010.1
CURRENT APPLICATION NUMBER: US/09/181,585
CURRENT FILING DATE: 1998-10-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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0.9%; Score 43.8; DB 4; Length 1159;
Best Local Similarity 47.0%; Pred. No. 0.013;
Matches 135; Conservative 0; Mismatches 152; Indels 0
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                                                                                                                                                                                                                                                                                                                                                       ) OTHER INFORMATION: Description of Artificial Sequence: cDNA; OTHER INFORMATION: comprising exons E, C, and A US-09-181-585-3
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Patent No. 6524791
GENERAL INFORMATION:
APPLICANT: Ranum, Laura P.W.
APPLICANT: Koob, Michael
                                                                                                                                                                                                                                                                    TYPE: DNA
ORGANISM: Artificial Sequence
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SOFTWARE: Patentin Ver. 2.0
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US-09-181-585-1/C
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1388 ACATCAAATAGTAAAATAAGATAATATATTTTAAAAAATGCAGCAGCAGCAGCAGCAGC
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APPLICANT: Dong Kyu JIN
TITLE OF INVENTION: Diagnostic Method and Kit for Meuropsychiatric Diseases
TITLE OF INVENTION: Using Trinucleotide Repeats Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     123 ACCTCACGGAAGAGGAGAAAATCATCCTGGCTGTCATGGATCGTCAGAAGAAGAAG 182
587
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                                                               303 AACCCAATGAGAAGGCCCCAGACAAAGCTGCACCAACAATTTGAAATGTATAAGGAGC 362
                                                                                                                            APPLICANT: Ranum, Laura P.N.
APPLICANT: Ranum, Michael
TITLE OF INVENTION: SPINOCERBELLAR ATAXIA TYPE 8 AND METHODS OF DETECTION
FILE REFERENCE: 11000901011
CURRENT APPLICATION NUMBER: US/09/181,585
CURRENT FILING DATE: 1998-10-28
NUMBER OF SEQ ID NOS: 18
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO. 2
LERGTH: 1471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            183 AGGAGAAGGAGCAGTCCGTGCTCAAGATCAAAGAAGAACAAAGCACAAAGCACACAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           243 GGTTTCCCTTTAGTGGGATCACTGAACTGGTAAATAACGTTCTGCAGCCCCAGCAAAAC
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0.9%; Score 43.8; DB 4; Length 1471;
Best Local Similarity 47.0%; Pred. No. 0.016;
Matches 135; Conservative 0; Mismatches 152; Indels 0.
                                                                                                                                                                                                                                                               526 AGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGTAGCAGTAIG 480
                                                                                                                                                                                                   363 AAGTCAAGAAGATGGGAGAATCGCAGCAGCAAGAAGAGCAGAAG 409
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; OTHER INFORMATION: Description of Artificial Sequence: cDNA; OTHER INFORMATION: comprising exons D, C, B, and A US-09-181-585-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILE REFERENCE: 1942/36
CURRENT APPLICATION NUMBER: US/09/253,691
CURRENT FILING DATE: 1999-02-22
EARLIER APPLICATION NUMBER: RR 98-6,278
EARLIER FILING DATE: 1996-02-26
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NS-09-410-5518-20
| Sequence 2.0 Application US/09410551B |
| Patent No. 6503737 |
| GENERAL INFORMATION: |
| PATENT NO. 6503737 |
| GENERAL INFORMATION: |
| PAPPLICANT: KOGAN BICSCIENCES, Inc. |
| APPLICANT: RADGLA, CHAITAN |
| APPLICANT: RADGLA, CHAITAN |
| APPLICANT: RADGLA, CHAITAN |
| APPLICANT: RADGLA, CHAITAN |
| APPLICANT: RADGLA, CHAITAN |
| APPLICANT: SANTI, DANIEL |
| APPLICANT: SANTI, DANIEL |
| APPLICANT: SANTI, DANIEL |
| APPLICANT: SANTI, DANIEL |
| TITLE OF INVENTION: POUNTRINCE THEREFOR |
| TITLE OF INVENTION: POUNTRINCE US 60/129, 810 |
| FRICA FILING DATE: 1999-06-17 |
| FRICA FILING DATE: 1999-06-17 |
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| FRICA FILING DATE: 1998-10-02 |
| FRICA FILING DATE: 1998-10-02 |
| FRICA FILING DATE: 1999-06-17 |
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| FRICA FILING DATE: 1998-10-02 |
| FRICA FILING DATE: 1998-10-02 |
| FRICA FILING DATE: 19
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3390 ATACAAACCTCATGAGGTCGATGCCTTCATTAATGACTGGAAGATCTGCCCCTCCTTCAC 3449

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332 ccaseracicascadadricacarcascadaerraradacarcricaracartecadad 391

272 ccdakccecedeccececedeckcacacakekecekecekenecekenesekandecene 331

3330 CAGAACAACGGCCTCTCCTAGAGCGGACCACCCCCCTCCAGATCCTCTGAACGTCCTG 3389

Query Match
0.9%; Score 42.4; DB 4; Length 4466;
Best Local Similarity 50.5%; Pred. No. 0.094;
Matches 103; Conservative 0; Mismatches 101; Indels 0

0; Gaps

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        Db
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        Db
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Search completed: December 11, 2003, 23:16:04 Job time : 309 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model Run on:

December 11, 2003, 20:44:17; Search time 2658 Seconds (without alignments) 6227.059 Million cell updates/sec

US-09-617-099B-2 4980

1 gcttccctagggtggttcgg.....acattgtgccctagcaaagg 4980 Perfect score: Sequence:

IDENTITY NUC Gapop 10.0 , Gapext 1.0 Scoring table:

2201672 seqs, 1661799599 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Published_Applications_NA:* Database :

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		*				
Result		Query				
No.	Score	Match	Match Length DB	DB	ID	Description
-	4980	100.0	4980	15	US-10-180-326-2	Semence 2. Appli
N	715	14.4	6638	13	US-10-220-891-40	Semience 40. And
m	398.2	8	7325	13	US-10-240-965-72	Semence 72. Appl
4	113.8	2.3	365	σ	US-09-864-761-4068	Sequence 4068. An
ហ	105.8	2.7	568	13	US-10-029-386-3580	Semience 3580. Ar
9 U	96.2	1.9	642	13	US-10-027-632-251328	Section 251328
7	96.2	1.9	642	14	US-10-027-632-251328	Samence 251328
80	95.2	1.9	2404	133	US-09-814-353-21052	Sections 21052 3
о О	80.4	1.6	219	6	US-09-864-761-21755	Semience 21755 A
10	76.8	1.5	169	10	US-09-728-445-246	Sections 246 Ann
11	69.8	1.4	153	o	US-09-864-761-20824	Semience 20824 A
12	65	1.3	65	13	US-09-908-975-27152	Semience 27152. A
c 13	54.4	1.1	369	0	US-09-864-761-5028	Semience 5028. An
14	52.8	1:1	104	13	US-10-029-386-17280	Sequence 17280. A
15	50.4	1.0	9	13	US-09-908-975-10530	Segmence 10530. A

Sequence 237. App	Sequence 237. App	110. 7	Sequence 110. App	45	Seguence 450. App	Sequence 446. App	448	65	161	168		-	228	212.	212	212	212	212	212	8 212.	212.	Sequence 212, App	212	212.	212.	8521		198.	198,	
US-09-764-870-237	U8-10-125-540-237	US-09-764-870-110	US-10-125-540-110	US-10-168-659-45	US-10-177-293-450	US-10-177-293-446	US-10-177-293-448	US-10-378-094-65	US-10-116-275-161	US-09-974-298-168	US-10-307-389-12	US-10-294-804-1	US-10-029-386-22859	US-10-140-472-212	US-10-141-761-212	US-10-142-885-212	US-10-158-790-212	US-10-137-871-212	US-10-140-805-212	US-10-140-864-212	US-10-140-923-212	US-10-141-756-212	US-10-141-759-212	US-10-123-155-212	US-10-146-731-212	U8-09-864-761-8521	US-10-140-472-198	US-10-141-761-198	US-10-142-885-198	
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ALIGNMENTS

APPLICANT: Seino, Susumu
APPLICANT: Shibasaki, Tadao
APPLICANT: Cozaki, No. US20030049661Aluaki
ITILE OF INVENTION: Protein Rim2
FILE REFERENCE: P21573
CURRENT APPLICATION NUMBER: US/10/180,326
CURRENT FILING DATE: 1990-10-08

PRIOR APPLICATION NUMBER: JP 288372/99
PRIOR FILING DATE: 1999-10-08
5

PRIOR FILING DATE: 1999-10-08
5

SOFTWARE: Patentin version 3.0
5

LENGTH: 4980 Sequence 2, Application US/10180326 Publication No. US20030049661A1 GENERAL INFORMATION: ; TYPE: DNA ; ORGANISM: Mus musculus US-10-180-326-2

1 GCTTCCCTAGGGTGGTTCGGCTCCGCCAAACATGTCGGCTCCGCTCGGCTCCGGGGCCC Gaps ó 100.0%; Score 4980; DB 15; Length 4980; 100.0%; Pred. No. 0; 0, Indels 0; Mismatches Query Match 100.0° Best Local Similarity 100.0° Matches 4980; Conservative

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1811 GAAGTGAATTTCTTGGAGAGATCCTCATAGAATTGGAAGAGAGGAGGAGGATGATGAA 2870
                                                                                                                                                                                                                                                                                   2691 AAGAAAATACTAGAACCAAAATGGAATCAAACTTTTGTCTATTCACATGTACATCGTAGA 2750
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                                                                                                                                                                  GTTAAGATTTACTTCCTTCCAGATAGAAGTGATAAAAATAAGAGAAGAACAAAAAGTC
                                                                            2531 ACAAITITIGGGAGCAAAGGATCTCCCTTCCAGGGAAGATGGGAAGGCCAAGGAATCCTTAT
                                                                                                     2571 ANTOTICHICAAGCAACAGATCTACTGCTAGAGTAGATGGACGTCCTCGAAATCCTTAT
                                                                                                                                                                                                                                                       2651 AAGAAAACTTIGGAACCCAAAIGGAACCAGACTTTCATTTATTCTCCTGTCCACGAAGA
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APPLICANT: SHIFMAN, Dov
APPLICANT: SHIFMAN, Dov
APPLICANT: SCHOOTI, Roland
APPLICANT: BOMOGY: Roland
APPLICANT: BOMOGY: ACIDANC
APPLICANT: BEILHAMER, Jeffrey J.
APPLICANT: MIXITA, Thomas
TITLE OF INVENTION GRNES EXPRESSED IN FOAM CELL DIFFERENTIATION
TITLE OF INVENTION NUMBER: US/10/240,965
CURRENT APPLICATION NUMBER: US/10/240,965
CURRENT APPLICATION NUMBER: 05/195,106
PRIOR PILING DATE: 2002-10-04
PRIOR PILING DATE: 2002-10-04
PRIOR PILING DATE: 2000-6-05
NUMBER OF SEQ ID NOS: 276
SOFTWARE: PERL PROGRAM
SEQ ID NO 72
LENGTH: 7325
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Publication No. US20030165924A1
GENERAL INFORMATION:
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ORGANISM: Homo sapiens
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                                                                                                                                 1668 ccacaccadacaradaccagaraccadaaaccccadaacrcaaaacccaadaccc 1727
                                                                                                                                                                             CTACGGAAACAGCACCACTTAGATCCCAGCTCTGCTGAGGAAAACGAAAGCGAGAAAA 1570
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AGAACTCGAGAGGCTCAGGGACAAAGTTCTTATCCACAAAGGACCTCAAAATCATAGTCCT
                                                                                                                                                                                                                                                                   1571 ATGGAAACCATGTTAAGGAATGATTCTTTGAGTTCAGACCAGTCCGAGTCAGTGAGGCCG
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                                                                                        CCCACCCTCGGCGGAGCCCTATACCGCTTGATAGACCAGAACATGAGGCGCGCTGACTCC
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APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Hanzel, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR PILLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
FILL APPLICANT: Acomica-X-1
                                                                                                                                                                                                                                               FILE REFERENCE: ABOMICAN-X-1
CURRENT AFFICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR PILING DATE: 2000-02-04
PRIOR FILING DATE: 2000-02-04
PRIOR FILING DATE: 2000-05-66
PRIOR PILING DATE: 2000-08-03
PRIOR PILING DATE: 2000-08-03
PRIOR PILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: US 60/236,356
PRIOR APPLICATION NUMBER: US 60/236,356
PRIOR PILING DATE: 2000-10-04
PRIOR PILING DATE: 2000-10-04
PRIOR PILING DATE: 2001-01-30
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NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No. US20030165924A1 977757.3
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ö ö Query Match 2.3%; Score 113%8; DB 9; Length 365; Best Local Similarity 72.2%; Pred. No. 8.5e-24; Matches 148; Conservative 0; Mismatches 57; Indels 0 HEXPRESED IN PLACENTA, SIGNAL = 2.9
REXPRESED IN ADULT LIVER, SIGNAL = 1.8
REXPRESED IN BONE MARROW, SIGNAL = 1.9
REXPRESED IN HELA, SIGNAL = 2.5
REXPRESED IN HELAO, SIGNAL = 2.1
REXPRESED IN HEART, SIGNAL = 2.1
REXPRESED IN HEART, SIGNAL = 2.1
REXPRESED IN HEART, SIGNAL = 2.1 EXPRESSED IN EXPRESSED EXPRESSED IN EXPRESSED EXPRES TYPE: DNA ORGANISM: Homo sapiens FEATURE:

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> Sequence 4068, Application US/09864761 RESULT 4 US-09-864-761-4068

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4086 CCGAAGGAGGAGATAAAAGCTACGGAGCACTGTTCAGAGAAAGCACGGAGACACCGGCTAG 4145
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FILE REFRENCE: 108927-129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT PILLING DATE: 2002-04-30
FRIOR APPLICATION NUMBER: US 60/218,006
FRIOR APPLICATION NUMBER: US 60/218,006
FRIOR PILLING DATE: 2000-04-20
FRIOR FILLING DATE: 2000-04-20
FRIOR FILLING DATE: 2000-04-20
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FRIOR FILLING DATE: 2000-03-29
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JAPPLICANT: Mang, David G.

TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827,129

CURRENT APPLICATION NUMBER: US/10/027,632

CURRENT PILING DATE: 2002-04-30

FRICH FLING DATE: 2000-04-20

FRICH FLING DATE: 2000-07-12

FRICH FLING DATE: 2000-07-12

FRICH FLING DATE: 2000-07-12

FRICH FLING DATE: 2000-03-29

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1.9%; Score 96.2; DB 13; Length (Best Local Similarity 83.4%; Pred. No. 3.6e-18; Matches 121; Conservative 0; Mismatches 23; Indels
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; Sequence 251328, Application US/10027632
; GENERAL INFORMATION:
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; ORGANISM: Ruman
US-10-027-632-251328
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APPLICANT: Rank, David R.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David R.
APPLICANT: Hanzel, David R.
TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
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TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
CURRENT APPLICATION NUMBER: 18/10/029,386
CURRENT FILING DATE: 2001-12-20
NUMBER OF SEQ ID NOS: 34288
SEQ ID NOS: 34288
SEQ ID NOS: 34288
LENGTHRE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 3580
                                                                                                                                                                                                                                                                                                                                                                                                                                  3957 GCCAGTCCGACACTGCAGTGGGCGCCCTGGGTACCAGTGGCAAGAAGCGGCGATCTAGCA 4016
                                                                                                                                                  3897 ACTTGACCAAAAGCACCAGCATCAGTGGAGACATGTGCTCACTGGAGAAGAATGACGGCA 3956
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       161 GTAAATATAGTTCATTTACCCCCAAAATGCAAGGCAGACGGATGGGGACTTCAGGAAGAT 220
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OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 0.81

OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.4

OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.4

OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1

OTHER INFORMATION: HIT: gil6306469, EVALUE 1.00e-111

OTHER INFORMATION: EST HUMAN HIT: BF951698.1, EVALUE 0.00e+00

US-10-029-386-3580
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Publication No. US20030204075A9
GENERAL INFORMATION:
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; Sequence 3580, Application US/10029386
; Publication No. US20030194704A1
; GENERAL INFORMATION:
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ORGANISM: Homo sapiens
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| Publication No. US20030165831A1
| GENERAL INFORMATION:
| APPLICANT: Lee, John
| APPLICANT: Thompson, Pamela
| APPLICANT: Thompson, Pamela
| APPLICANT: Thompson, Pamela
| APPLICANT: Inlie, James
| APPLICANT: Thompson, Pamela
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| APPLICANT: Thompson, Pamela
| TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
| TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
| TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
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| TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
| TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
| FRIOR PAPLICATION NUMBER: US 60/207,124
| PRIOR FILING DATE: 2000-06-15
| PRIOR FILING DATE: 2000-06-15
| PRIOR FILING DATE: 2000-06-15
| PRIOR FILING DATE: 2000-06-15
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| PRIOR FILING DATE: 2000-07-25
| PRIOR FILING DATE: 2000-06-15
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1.9%; Score 95.2; DB 13; Length 2404;
Best Local Similarity 87.9%; Pred. No. 2e-17;
Matches 116; Conservative 0; Mismatches 13; Indels 3;
                                                                                                          Query Match
1.9%; Score 96.2; DB 14; Length 642;
Best Local Similarity 83.4%; Pred. No. 3.6e-18;
Matches 121; Conservative 0; Mismatches 23; Indels 1
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| LOCATION: 1, 2404
| COTHER INFORMATION: n = A,T,C or G
US-09-814-353-21052
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ORGANISM: Homo sapiens
; ORGANISM: Human
US-10-027-632-251328
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3930 TGTGCTCACTGGAGAAGAATGACGGCAGCCAGTCCGACACTGCAGTGGGCCCCCTGGGTA 3989
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OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 2.9
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.8
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.9
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 2.5
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 2.1
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 2.2
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 2.3
OTHER INFORMATION: EXPRESSED IN LIVER, SIGNAL = 2.3
OTHER INFORMATION: EXPRESSED IN LIVER, SIGNAL = 2.3
OTHER INFORMATION: EXPRESSED IN LIVER, SIGNAL = 2.3
OTHER INFORMATION: EXPRESSED IN LIVER, SIGNAL = 2.3
OTHER INFORMATION: EXPRESSED IN LIVER, SIGNAL = 2.3
OTHER INFORMATION: EXPRESSED IN LIVER, SIGNAL = 2.3
OTHER INFORMATION: EXPRESSED IN LIVER, SIGNAL = 2.3
OTHER INFORMATION: STRESSED IN LIVER, SIGNAL = 2.3
OTHER INFORMATION: STRESSED IN LIVER, SIGNAL = 2.3
OTHER INFORMATION: STRESSED IN LIVER, SIGNAL = 2.3
OTHER INFORMATION: STRESSED IN LIVER, SIGNAL = 2.3
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1.4%; Score 69.8; DB 9; Length 153;
Best Local Similarity 69.8%; Pred. No. 1.7e-10;
Matches 111; Conservative 0; Mismatches 42; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 caggregaaagaaaceaaaarccaeccrraereccaaagregrregearae
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                                               CURRENT FILING DATE: 2001-05-23

PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR APPLICATION NUMBER: US 60/207,456

PRIOR FILING DATE: 2000-02-26

PRIOR FILING DATE: 2000-03-26

PRIOR PLING DATE: 2000-03-27

PRIOR PLING DATE: 2000-03-27

PRIOR PLING DATE: 2000-03-27

PRIOR PLING DATE: 2000-03-27

PRIOR PLING DATE: 2000-03-27

PRIOR PLING DATE: 2000-03-27

PRIOR PLING DATE: 2001-03-30

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Patent No. US20020048763A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL OF INVENTION:
APPLICANT: Rank, David R.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: GENER EXPRESSION ANALYSIS BY MICROARRAY
FILE REPERENCE: Aeomica-X-1
                                                                                                                                                                                                                                                                                                                                     4647 TACTCTTAGATGAACTGGAACTATCCAACATGGTGATTGGATGGTTCAAACTCTTCCCTC 4706
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4707 CTTCCTCCCTAGTAGATCCAACCTCGGCACCTCTGACAAGAAGAGCTTCCCAATCGTCTC 4766
                                                                                                                                                                     4587 TCATTGTCTGGGGAGATTATGGTCGTATGGATCACAAATCCTTTATGGGAGTGGCCCAGA 4646
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                                                                                                                                                                                                                                                                                                                                                                                                  158 TGCTGCTGCAGAGGTGCAGCTTGACCACCCTGGCCGTGGGCTGGTACAGCTCTTCCCCA 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-728-445-246

Sequence 246, Application US/09728445

Patent No. US20020102543A1

GENERAL INFORMATION:
APPLICANT: Friedrich, Glenn
APPLICANT: Zambrowicz, Brian
APPLICANT: Sands Arthur T.
TITLE OF INVENTION: No. US20020102543A1e1 Mutated Mammalian Cells and
TITLE OF INVENTION: Animals
FILE REFERENCE: LEX-0102-USA
CURRENT FILING DATE: 2000-11-30
PRIOR PLING DATE: 1999-12-01
PRIOR PLING DATE: 1999-12-01
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 246
LENGTH: 169
TYPE: DNA
CREANISM: Mus musculus
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        Length 219;
                                                                                           86; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TGGAAAGTTCTACCGGACCTTCTTACTCTCGTTCATAG 4804
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Query Match 1.6%; Score 80.4; DB 9;
Best Local Similarity 60.6%; Pred. No. 1.2e-13;
Matches 132; Conservative 0; Mismatches 86
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; OTHER INFORMATION: n = A,T,C or G
US-09-728-445-246
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윱 Š Gaps

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GENERAL INFORMATION:
APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXCH NUCLEIC ACID PROBES USEFUL FOR
TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
FILE REPRENCE: ASOMICA-K-2
CURRENT APPLICATION NUMBER: US/10/029,386
CURRENT FILING DATE: 2001-12-20
NUMBER OF SEQ ID NOS: 34288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1713 CCCTAGTAGATCCAACCTCGGCACCTCTGACAAGAAGAGCTTCCCGAATCGTCTCTGGAAA 4772
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1.1%; Score 54.4; DB 9; Length 369;
Best Local Similarity 59.9%; Pred. No. 1.9e-05;
Matches 91; Conservative 0; Mismatches 61; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA

ORGANISM: Homo sapiens
FRATURE:

OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.93

OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.3

OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.3

OTHER INFORMATION: EXPRESSED IN HELLOO, SIGNAL = 1.5

OTHER INFORMATION: EXPRESSED IN HELLOO, SIGNAL = 1.6

OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.7

OTHER INFORMATION: EXPRESSED IN HEACH, SIGNAL = 1.6

OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.6

OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.6

US-09-864-761-5028
                                                                              PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR PLING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR PLING DATE: 2001-01-30
PRIOR PLING DATE: 2001-01-30
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PRIOR PLING DATE: 2001-01-30
PRIOR PLING DATE: 2001-01-30
PRIOR PLING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SEQ ID NO S: 49117
SEQ ID NO S: 49117
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                                                                    PCT/US01/00669
         PCT/US01/00664
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Publication No. US20030194704Al:
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APPLICANT: WASSERMAN, Alon
APPLICANT: WINTZ, Eli
APPLICANT: MINTZ, Liat
APPLICANT: MINTZ, Liat
APPLICANT: MINTZ, Liat
APPLICANT: MINTZ, Liat
APPLICANT: MINTZ, Liat
APPLICANT: MINTZ, Liat
APPLICANT: MINTZ, Liat
APPLICANT: MINTZ, Liat
APPLICANT: PAIGLER, Simchon
TITLE OF INVENTION: THAT POPULATE A TRANSCRIPTS AND SPLICE
TITLE OF INVENTION: THAT POPULATE A TRANSCRIPTOME
FILE REFERENCE: 3668-0005
CURRENT APPLICATION NUMBER: US 60/287,724
PRIOR FILING DATE: 2000-07-28
PRIOR APPLICATION NUMBER: US 60/221,607
PRIOR APPLICATION NUMBER: US 60/221,607
PRIOR SEQ ID NOS: 32337
SOFTWARE: PATENTIN VERSION 3.0
SEQ ID NO 2152
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VES-09-864-761-5028/C

Sequence 5028, Application US/09864761

FREARI NO. USZO020048763A1

FREARI NO. USZO020048763A1

FREARI LINFORMATION:

APPLICANT: Penn, Sharron G.

APPLICANT: Hanzel, David R.

APPLICANT: Chen, Wensheng

TITLE OF INVENTION: HUMBER US/09/864,761

TITLE OF INVENTION: HUMBER: US/09/864,761

CURRENT PAPLICATION NUMBER: US/09/864,761

CURRENT FILING DATE: 2001-05-23

FRIOR APPLICATION NUMBER: US 60/180,312

FRIOR APPLICATION NUMBER: US 60/207,456

FRIOR PILING DATE: 2000-05-26

FRIOR FILING DATE: 2000-05-36

FRIOR FILING DATE: 2000-06-36

FRIOR FILING DATE: 2000-06-36

FRIOR APPLICATION NUMBER: US 60/207,456

FRIOR PILING DATE: 2000-05-36

FRIOR PILING DATE: 2000-06-37

FRIOR APPLICATION NUMBER: US 60/236,356

FRIOR APPLICATION NUMBER: US 60/236,359

FRIOR PILING DATE: 2000-09-27

FRIOR PILING DATE: 2000-09-27

FRIOR PILING DATE: 2000-09-27

FRIOR PILING DATE: 2000-09-27

FRIOR PILING DATE: 2000-09-27
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Pred. No. 2.7e-09;
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4050 CACGGAAAAGTCGCAGTGCCTCTCAACTCAGCCAAACCG 4088
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1.3%; Score 65; DB
Best Local Similarity 100.0%; Pred. No. 2.7
Matches 65; Conservative 0; Mismatches
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FILING DATE: 2001-01-30
                                                                                                                                                                                                        ; Sequence 27152, Application US/09908975; Publication No. US20030165843A1; GENERAL INFORMATION;
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ORGANISM: Mus musculus
US-09-908-975-27152
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Sequence 10530, Application US/09908975

Publication No. US20030165843A1

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FRIOR APPLICATION NUMBER: OS 0221,607
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SOFTWARE: Patentin version 3.0
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Best Local Similarity 69.2%; Pred. No. 2.3e-05;
Matches 72; Conservative 0; Mismatches 32; Indels 0
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OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.5

OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.81

OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.4

OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.

OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.

OTHER INFORMATION: TIT: gil4755927, EVALUE 6.00e-52

OTHER INFORMATION: EXT.HUMAN HIT: AN956936.1, EVALUE 9.00e-52
US-10-029-386-17280
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1.0%; Score 50.4; DB 13; Length 60;
Best Local Similarity 90.0%; Pred. No. 8.2e-05;
Matches 54; Conservative 0; Mismatches 6; Indels
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Mus musculus adult male hippocampus CDNA, RIKEN full-length enriched library, clone:C630023321 product:Rab3 interacting protein 1, full insert sequence.
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Itoh, M., Komo, H., Okazaki, Y., Muramatsu, M., and Hayashizaki, Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes
Genome Res. 10 (10), 1617-1630 (2000)
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Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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L. Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research Group, Mixen Genome Exploration Research Group, Mixen Genome Exploration Research Group, Rikk Genome Skiploration Session (16-APR-2016) Teurumi-ku, Yokohama, Walnagawa 230-0045, Japan (8-mail:genome-res@gec.riken.go.jp, Tel:81-45-503-9222, Prax:81-45-503-9216)
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Group Phase I & II Team.

Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

Nature 420, 563-573 (2002)
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Nature 409 (6821), 685-690 (2001)
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URL:http://fantom.gsc.riken.go.jp/
Location/Qualifiers
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The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.

Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

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Return 420, 563-573 (2002)

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DEGEGGGKKLRSTVQRSTETGLAVEMRNWMTRQAGRRSTDGSMNSYSSBGNLIFPGVR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CDNA library was prepared and sequenced in Wouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.

Please vist our web site for further details.

Please vist our seb site for further details.

URL:http://genome.gsc.riken.go.jp/.

Location/Qualifiers.
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/clone_lib="RIKEN full-length enriched mouse cDNA library"
/dev_stage="adult"
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/mol_type="mRNA"
/strain="C57BL/G1"
/db_xref="FANTOM_DB:6430709C16"
/db_xref="taxon:1099"
/clone="6430709C16"
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Mus musculus adult male olfactory brain cDNA, RIKEN full-length enriched library, clone:6430709C16 product:Rab3 interacting protein 1, full insert sequence.
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                                                                                                                                             1070 TCCCTACGGAAACAGCACCACTTAGATCCCAGCTCTGCTGTGAGGAAAACGAAGGACAA 1129
                                                                                                                                                                                                                                                                                              1568 AAAATGGAAACCATGTTAAGGAATGATTCTTTGAGTTCAGACCAGTCCGAGTCAGTGAGG 1627
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Suni, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Pujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, S., Watshik, M., Yoneda, Y., Muramatsu, M., Inoue, Y., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramstsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y. sequencing pipeline with 384 multicapillary sequencer Gennat Genome Res. 10 (11), 1757-1771 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1688 AGCAGCTCGGAGGAGGAGCTGGCATCCACACCTGAGTATACAAGCTGTGATGATGATGAGGAG 1747
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Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
99279253
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AK032619.1 GI:26328428
HTC; CAP trapper.
Mus musculus (house mouse)
Mus musculus
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Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/Likit at: http://image.llnl.gov Series: IRAK Plate: 32 Row: b Column: 12.

This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 7662285

This clone has the following problem: frame shifted.

Location/Qualifiers

1. .1200
/organism="Homo sapiens"
/mol Lype="mRNA"
/db xref="taxon:9806"
/clone="INAGE:4792768"
/lisue type="Brain, hypothalamus"
/clone="INAGE:4792768"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: MGC help desk

Bmail: cgaphs-r@mail.nh.gov

Tissue Procurement: Miklos Palkovite, M.D., Ph.D.

Tissue Procurement: Miklos Palkovite, M.D., Ph.D.

Toshlyuki and Piero Carninci (RIKES)

Toshlyuki and Piero Carninci (RIKES)

DNA Sequencing by: The I.M.A.G. Consortium (LIML)

DNA Sequencing by: Sequencing Group at the Stanford Human Genome Center, Stanford University School of Medicine, Stanford, CA 94305

Web site: (Dickson, Mark) mcd@paxil: stanford.edu

Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           242 Addahadandcccarcrorrorcandarcadaaradahadaracahccanceanda 301
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                                                                                                                                                                                                                                                                                                                                                                                                                Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

    (bases 1 to 1200)

1197 GATACCAAGCAGTCCTGTGTTCTCAGAGGAAGTCGTACACATTGTGCCCTAGCAAAGG 1254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Direct Submission
Submitted (03-DEC-2001) Mational Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            848 AGRARACGRAGTCCRTCTCCRGGGATCRARATCGRACATACGRACCAAACTCAAGAA
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                                                                                                                                    Homo sapiens, Similar to KIAA0751 gene product, clone IMAGE:4792768, mRNA.
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Pred. No. 1.3e-148;
0; Mismatches 123; Indels
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BC018057.1 GI:17390117
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832; Conservative
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Homo sapiens
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                             GSKTLPAPYVKVYLLDNGVCIAKKKTKVARKTILRPLYQQLLSFEBSPQGKVLQIIVWG
DYGRMDHKSFMGVAQILLDELELSNMVIGWFKLPPPSSLVDPTLAPLTRRASQSSLBS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1263 ACAGCCAGTTCAGTGATTTCCTGGATGGCCTGGGCCCTGCTCAGCTAGTGGGACGCCAGA 4322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CCCTGGCTACTCCTGCAATGGGTGACATTCAGGTGGGAATGATGGATAAAAAGGGACACAGC 4382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TGGAGGTAGAAATCATCCGGGGGGGGGCGTTGTGGTAAAACCAGGTTCCAAGACACTGC 4442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4622
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4802
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1137 GGTGGAAGCCCCTGGTAACACTGCATGCTTGATGTCTACAGAGCCCACGTCTAGG 1196
LASDSQPSDFLDGLGPAQLVGRQTLATPANGDIQVGMMDKKGQLEVEIIRARGLVVKP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GGTGGAAGCCCCTGGTAACACTGCATGCTTGATGTTGTGTCTACAGAGCCCACGTCTAGG 4922
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           656
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       357 AAGGAGAAGAAGAAGTAAAAAGCTACGAAGCACTGTTCAGAGAAGCACGGAGACCGGGC 416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           477 GCATGAACAGCTATAGCTCGGAAGGAAATCTGATCTTCCCTGGGGTCCGCCTGGCCTCTG 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          537 ACAGCCAGTTCAGTGATTTCCTGGATGCCTGGCCCTGCTCAGCTAGTGGGACCCCAGA 596
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       897 AATCCTTTATIGGGAGTIGGCCCAGATACTCTTAGATGAACTGGAACTATCCAACATGGTGA 956
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GATACCAAGCAGTCCTGTGTTCTCAGAGGAAGTCGTACACATTGTGCCCTAGCAAAGG 4980
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TAGCAGTGGAGATGAGGAACTGGATGACCCGGCCAGGCCGGGAATCCACAGATGGCA
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                                                                                                                                                                                                                                                                                                                                                                                                             0; Gaps
                                                                                                                                                                                                                                                                                                                                           Score 891.6; DB 11; Length 3687;
Pred. No. 1.4e-176;
0; Mismatches 4; Indels 0; G
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/note="putative"
3687
                                                                                                                                                                                                                   note="putative"
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Best Local Similarity 99.6%;
Matches 894; Conservative
                                                                                         STGPSYSRS
                                                                                                                                                                                                                                                 825 C
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Y., Shibata, K., Itoh, M., Carninci, P., Sugahara
                                                                                        nods for the mouse full-length cDNA
time sequence clustering for construction of a
lbrary. Genome Res. . 11 (2), 281-289 (2001)
s.A., Saito, T., Kiyosawa, H., Yamanaka, I., Aizawa
a.A., Itoh, M., Kawai, J., Shibata, K. and
quence analysis (RISA) system--384-format with 384 multicapillary sequencer. Genome Res. 2000)
                                                                                                                                                                                                                                                                          pared and sequenced in Mouse Genome tof Genome Exploration Research Group in Riken iter and Genome Science Laboratory in RIKEN. ental Animal Research in Riken contributed to
                                                                                                                                                                                                     rais of Full-Length Mouse cDNAs Compared with
tes Mamm. Genome. 12, 673-677 (2001)
bb site (http://genome.gsc.riken.go.jp/) for
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 682.4; DB 10; Length 686;
Pred. No. 1e-132;
0; Mismatches 3; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 e="hippocampus"
"adult"
                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus"
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mol_type="mRNA"

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1388 GAAAGAACTCGAGAGGCTCAGGGACAAAGTTCTTATCCACAAAGGACCTCAAATCATAGT 1447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1148 TACAGAAGTGATCCCAAATCTGGCCCGGTATCCCGTAAAGCCACAACCCTACGAAGAACAA 1207
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     This clone was contributed by the Brain Molecular Anatomy Project (BMAP)
Seq primer: PYX-5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   848 AGNARACGRAGTCCATCAGGGTCCAGGGATCCAAGGATACGAGCAAAGTCAAAAA 907
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   97 AGAAAACGAAGTCCATCAGTCTCCAGGGATCAAAATCGAGATACGAGCAAAGTGAAGAA 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AGAGAGGACTACTCACAGTATGTTCCTTCAGATGGTACAATGCCAAGATCTCCTTCGGAT 967
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 157 AGAGAGGACTACTCACAGTATGTTCCTTCAGATGGTACAATGCCAAGATCTCCTTCGGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TACAGAAGTCCCCAATCTGGCCCGGTATCCCGTAAAGCCACACACCCTACGAAGAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           tch 13.6%; Score 678; DB 14; Length 799; al Similarity 99.3%; Pred. No. 8.9e-132; 700; Conservative 0; Mismatches 3; Indels ;
                                                                                                                                      organism="Mus musculus"
                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
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1399 AGAGGCTCAGGGACAAAGTTCTTATCCACAAAGGACCTCAAATCATAGTCCTCCCCACCC 1458
                                                                                                                                                                                                                     CGCTGAGGTGTCCAGGGCACACAAGAAGGAACAGTGATGTTTCTTTGGCAAACGC 1278
                                                                                                                                                                                                                                                                                                                         TGTATCTGAACGTAGAGCTGCAATGGAAAACCAACGATCGTATTCAATGGAAAGAACTCG 1398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1459 TCGGCGGAGCCCTATACCGCTTGATAGACCAGACATGAGGCGCGCTGACTCCCTACCGAA 1518
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                                                                                                                                                                                                                                              241 TGTATCTGAAGGTAGAGCTGCAATGGAAAACCAAGGATCGTATTCAATGGAAAGAACTCG 300
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Email: cgapbs-remail.nih.gov
Tissue Procurement: Dr. Jim Lin, University of Iowa
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
CLONE Distribution: Distribution information can be found at
http://genome.uiowa.edu/distribution/mousefl.html
                                                                                                                                                            61 réchabitérdécédégraficedégrandecedenacetraceangandantique 120
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Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.

    (bases 1 to 799)

                                                                                                       TCCAAATCTGGCCCGGTATCCCGTAAAGCCACAACCCTACGAAGAACAAATGGCATCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1579 CATGTTAAGGAATGATTCTTTGAGTTCAGACCAGTCCGAGTCAGTGAGGCCGCCCCCACC
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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
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MIN-WGC http://wgc.nci.nih.gow/.

Mational Institutes of Health, Mammalian Gene Collection (MGC)

Mational Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished

Contact: Robert Strausberg, Ph.D.

Smail: cgapbs-r@mail.nih.gow

Tissue Procurement: The Cepko Laboratory

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: WGC clone distribution information can be thtp://mage.lih.gow

Plate: LiAM.4038 row: e Column: 18

High quality sequence stop: 571.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AGENCOURT 8929724 NIH_MGC_94 Mus musculus cDNA clone IMAGE:6489689 5', mRNA sequence.
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Mammalia; Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.

    (bases 1 to 1073)

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                                                                                        1508 TCCCTACGGAAACAGCACCTTAGATCCCAGCTCTGCTGTGAGG 1552
                                                                                                          Mus musculus (house mouse)
                                                                                                                                                                                                                                              BU502896.1 GI:22808299
                                                                                                                                                                                                                                                                                       Mus musculus
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1. (Dases 1 to 698)

NHH-MCC http://mgc.nci.nlh.gov/.

NHH-MCC http://mgc.nci.nlh.gov/.

In Unpublished
Contact: Robert Strausberg, Ph.D.

Emali: cgapbe-rémail.inih.gov
Tissue Procurement: Dr. Jim Lin, University of Iowa cDNA Library preparation: Dr. M. Bento Soares, University of Iowa CDNA Library Preparation: Dr. M. Bento Soares, University of Iowa DNA Sequencing by: Dr. M. Bento Soares, University of Iowa Clone Distribution: Distribution information can be found at http://genome.uiowa.edu/distribution/mousefi.html
This clone was contributed by the Brain Molecular Anatomy Project (BMAP)
                                                                                                                                                                                                                                                                                                                               1510
                                                                               1331 CAAAGATCTGTATCTGAACGTAGAGCTGCAATGGAAACCAACGATGCTATTCAATGGAA 1390
241 CAAAGATCTGTATCTGAACGTAGAGCTGCAATGGAAAACCAACGATGTATCAATGGAA 300
                                                                                                                                                                                                                  1450
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360
                                                                                                                                                                                                                                                                                                                                              361 CCCACCCTCGGCGGAGCCTATACCGCTTGATAGACCAGACATGAGGCGCGCTGACTCC 420
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/mol_type="mRNA"
/strain="C57BL/6"
/db_xref="taxon:10090"
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ISM Mus musculus

Rukaryota; Metazoa; Chordata; Craniata; Vertebrata; Ruteleostomi;

Rukaryota; Metazoa; Chordata; Craniata; Vertebrata; Ruteleostomi;

Rainla; Rutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 665)

Rainland Institutes of Health, Mammalian Gene Collection (MGC)

National Institutes of Health, Mammalian Gene Collection (MGC)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail: nih.gov

Tissue Procurement: The Cepko Laboratory

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.B. Consortium (LIML)

DNA Sequencing by: Incyte Genomics, Inc.

CONG Library Arrayed by: The I.M.A.G.B. Consortium/LiML at:

Cond distribution: MGC clone distribution information can be found through the I.M.A.G.B. Consortium/LiML at:

High quality sequence stops: 648.

Rish quality sequence stops: 648.
                                                                                                                                                                       BG296106 665 bp mRNA linear EST 21-FEB-2001
602393787F1 NIH_MGC_94 Mus musculus cDNA clone IMAGE:4505661 5',
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/lab host="DHIDB (phage-resistant)"
/clone_lib="NIH MGC 94"
/note="Organ: eye; Vector: pCNV-SPORT6; Site_1: Not1;
Site_2: Sall; Cloned unidirectionally; oligo-dT primed.
Average insert aize 3: 3. bb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH MGC Library."
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Pred. No. 4.9e-113;
0; Mismatches 2; Indels 3;
                  660 AACGANGCGAGAAAAATGGAAACCATGINTAGGAATGA 698
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/organism="Mus musculus"
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|db_xref="taxon:10090"
|clone="IMAGE:4505661"
                                                                                                                                                                                                                                                                                                                                                           Mus musculus (house mouse)
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Best Local Similarity 99.2
Matches 623; Conservative
                                                                                                                                                                                                                                mRNA sequence.
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                                                                                                                                                                                                                                                            ACCESSION
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/clone="IWAGE: 6850773"
/tissue_type="whole brain"
/dev stage="whole brain"
/dev stage="mbryo 13.5,14.5,16.5,17.5dpc"
/lab host="DH108 (TI phage resistant)"
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/clone_lib="NIH_EMAP_EYO"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1256 AGTGATGTTTCTTTGGCAAACGCTGAACTAGAAGATTCCAGGATTTCTCTCTGCTAAGGATG 1315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1016 GGTCATTTAAATTACAGGGATTCTAACAGGAGGGCCATAGACATTCCAAAGAGTATATT 1075
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1136 TACCAGGCACGCTACAGAAGTGATCCAAATCTGGCCCGGTATCCCGTAAAGCCACAAACCC 1195
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1495 GAGGCGCTGACTCCCTACGGAAACAGCACCACTTAGATCCCAGCTCTGCTGAGGAA 1554
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        896 CAAAGIGAAGAAAGAGAGACIACICACAGATAGIICCITCAGAIGGIACAAIGCCAAGA 955
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 TCTCCTTCOGATTATGCTGATAGACGATCTCAGCGTGAGCCTCAACCTTAGAAGAACCT 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               301 TACGAAGAACAAATGCGCATCCACGCTGAGGTGTCCAGGGCACGACGACGAGGCAC 360
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Best Local Similarity 99.14
Matches 693; Conservative
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/strain="C57BL/6"
/do_xref="taxon:10090"
/dow xstg="taxon:10090"
/clone="U1-M-D72-bM--p-02-0-U1"
/tissue_type="subfornical organ and postrema"
/dev stage="Adnit"
/lab_host="Most = "Most = "Most = "Most = "Most = "Most = "Most = "Most = "Most = "Most = "Most = "Most = "Most = "Most = "Most = "Most = "Most = "Most = "Most = "Most = "Most = "Most = "Most = "Most = "Most = "Most = "Most = "Most = "Most = "Most = "Most = "Most = "Most = "Most = "Most = "Most = "Most = "Most = "Most = "Most = "Most = "Most = "Most = "Most = "Most = "Most = "Most = "Most = "Most = "Most = "Most = "Most = "Most = "Most = "Most = "Most = "Most = "Most = "Most = "Most = "Most = "Most = "Most = "Most = "Most = "Most = "Most = "Most = "Most = "Most = "Most = "Most = "Most = "Most = "Most = "Most = "Most = "Most = "Most = "Most = "Most = "Most = "Most = "Most = "Most = "Most = "Most = "Most = "Most = "Most = "Most = "Most = "Most = "Most = "Most = "Most = "Most = "Most = "Most = "Most = "Most = "Most = "Most = "Most = "Most = "Most = "Most = "Most = "Most = "Most = "Most = "Most = "Most = "Most = "Most = "Most = "Most = "Most = "Most = "Most = "Most = "Most = "Most = "Most = "Most = "Most = "Most = "Most = "Most = "Most = "Most = "Most = "Most = "Most = "Most = "Most = "Most = "Most = "Most = "Most = "Most = "Most = "Most = "Most = "Most = "Most = "Most = "Most = "Most = "Most = "Most = "Most = "Most = "Most = "Most = "Most = "Most = "Most = "Most = "Most = "Most = "Most = "Most = "Most = "Most = "Most = "Most = "Most = "Most = "Most = "Most = "Most = "Most = "Most = "Most = "Most = "Most = "Most = "Most = "Most = "Most = "Most = "Most = "Most = "Most = "Most = "Most = "Most = "Most = "Most = "Most = "Most = "Most = "Most = "Most = "Most = "Most = "Most = "Most = "Most = "Most = "Most = "Most = "Most = "Most = "Most = "Most = "Most = "Most = "Most = "Most = "Most = "Most = "Most = "Most = "Most = "Most = "Most = "Most = "Most = "Most = "Most = "Most = "Most = "Most = "Most = "Most = "Most = "Most = 
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Contact: Chin, H
National Institute of Mental Health
(6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD
20892-9643, USA
Tel: 301 443 1706
Fax: 301 443 9890
Email: mEsr@mail.nih.gov
Tissue Procurement: Dr. Robin Davisson
CDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Researchers may obtain clones from Research
Genetics (Www.resgen.com).
Seq primer: M3 REVERSE.
                                                          CCTAGTAGATCCAACCTCGGCACCTCTGACAAGAAGTTCCCAATCGTCTTGGAAAG 4773
                                                                                                                                                                            TICTACCOGACCTTCTTACTCTCATAGCAACTATAAAACTGTTGTCACAACAACCA 4833
                                                                                                                                                                                                                                                                                              4834 GCGATA-CAAAAACCCAGAAGAAAACGCACAGGTGGAAGCCCCCTGGTAACACTGCATGCTT 4892
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UI-M-DJ2-bwj-p-02-0-UI.rl NIH BMAP_DJ2 Mus musculus CDNA clone.....UI-M-DJ2-bwj-p-02-0-UI 5', mRNA sequence.
                                                                                                                                                                                                                              TTCTACCGGACCTTCTTACTCTCGTTCATAGCAACTATAAAACTGTTGTCACAAAAACCA 479
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                                                                                                                                                                                                                                                                                                                                                                     539
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Bonaido,M.F., Jennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene
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stranded cDNA was ligated to an ECOR I adaptor, digested with Not I, and cloned directionally into pT773-Pac vector. The oligomucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is: GCTACATGAT, subformical sorgan and area postrema.
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1 (bases 1 to 697)
Bonaldo, M.F., Lennon, G. and Soares, M.B.
Normalization and subtraction: two approaches to facilitate gene
                                                                                                                                                                                                                                                                                                                                                                       4383 TGGAGGTAGAAATCATCCGGGGGGGGGGCCTTGT-GGTAAAACCAGGTTCCAAGACACTG
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697 bp mRNA linear EST 10.
UI-E-E01-aiz-h-20-0-UI.81 UI-E-E01 Homo sapiens cDNA clone
UI-E-E01-aiz-h-20-0-UI 3', mRNA sequence.
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                                                                                                                                                                                                                                                                                13; Length 594;
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11.7%; Score 580.4; DB 13
Best Local Similarity 99.7%; Pred. No. 2.8e-111;
Matches 592; Conservative 0; Mismatches 1;
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Genome Res. 6 (9), 791-806 (1996)
97044477
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Homo sapiens
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CCTCCTTCCTCCTCCTAGTAGATCCAACTCGGGACCTCTGACAAQAAGAGCTTCCCAATCG 4762
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Gallus gallus

Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,

Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,

Phasianinae, Gallus.

1 (Dases 1 to 944)

Boardann, P. B., Sanz-Ezquerro, J., Overton, I.M., Butt, D.W., Bosch, E.,

Rong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J.

A Comprehensive Collection of Chicken onwas

Curr. Biol. 12 (22), 1965-1969 (2002)
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/lab_host="DH10B"
/lab_host="DH10B"
/clone lib="CSEQCHL24"
/note="Organ: brain, Vector: pBluescript II KB(+); Site 1:
BCORI; Site 2: Not!; Modification of pBluescript II KB(+)
[Stratagene] vector to accommodate cDNA produced with the
Intimmed protocol (Construction of uni-directionally
cloned cDNA libraries from messenger RNA for improved 3'
end DNA sequenching by Glenn Ru; et al. U.S. Patent # 6,387,
624). Cut pBluescript II KB(+) with NotI and BCORI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BU140296 944 bp mRNA linear EST 25-NOV-2002 603134665F1 CSEQCHL24 Gallus gallus cDNA clone ChEST116b17 5', mRNA
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University of Manchester Institute of Science and Technology (UMIST
         397 TATCTATAGATAACGGAGTCTGCATAGCCAAAAAGAAAAGAAAAGGGGAAAAAACG 338
                                                                                                                                                                                                                                                                                                                                                                                217 CAGATACITITAGATGAACTAGAGCTATCCAATATGGTGATGGGTGTCAAACTTTTC 158
                                                                                                                                                                                              337 CTGGAACCCTTTACCAGCGGCTATTATCTTTCGAAGAGGTCCACAAGGAAAAGTTTTA
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Location/Qualifiers
1. 944
/ organism="Gallus gallus"
/ mol_type="mRNA"
/ strain="White Leghorn, Hisex"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PO Box 88, Manchester, M60 1QD, UK
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/clone="ChBST116b17"
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Fax: 01612360409
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AUTHORS
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// prognisma="Homo sapiens"
// db_tree="trex-aron:960"
// clone="tree="trex-aron:960"
// clone="tree="trex-aron:960"
// dev_tree="trex-aron:960"
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                               Contact: Soares, MB
Contact: Soares, MB
Continated Laboratory for Computational Genomics
University of Iowa
375 Newton Road, 4156 MEBRP, Iowa City, IA 52242, USA
7e1: 319 335 8250
Rax: 319 335 9565
Raxi: Dento-Soares@uiowa.edu
Tissue Procurement: Dr. Gregg Hageman
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Researchers may obtain clones from Research
Seq primer: M13 FORWARD
POLYA-Yes:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          638
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GCCCGTGGCCTTGTAAAACCAGGTTCCAAGACACTGCCAGCACCGTATGTAAAAGTG 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4224 AAGGAAATCTGATCTTCCCTGGGGTCCGCCTGGCCTCTGACAGCCAGTTCAGTGATTTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4165 GATGACCCGCCAGCCAGCCGGAATCCACAGATGGCAGCATGAACAGCTATAGGTC-GG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             697 dardacrodacadedaadeceaadereracadarderaceardaacaderaceade
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         637 AAGGAAATCTGATTTTCCCTGGTTTCGCTTGGCCTCTGATAGCCAGTTCAGTGATTTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1284 TGGATGGCCTGGCCCTGCTCAGCTAGTGGGACGCCAGACCCTGGCTACTCCTGCAATGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4344 GTGACATTCAGGTGGGAATGATGGTAAA-AAGGGACAGCTGGAGGTAGAAATCATCCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4403 GCGCGCCCTTGTGGTAAAACCAGGTTCCAAGACACTGCCAGCACCGTATGTCAAGGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 13; Length 697;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 others
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        212 t
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TAG_TISSUE=human fetal eye
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TAG_SEQ=CGCGTATACC"
161 c 159 q
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Standard; RNA; EST; 603

Homo sapiens mRNA; BST DKFZp686F14203_s1 (from clone DKFZp686F14203)

Created) Last updated, Version 1)

09-MAY-2003 (Rel. 75, 09-MAY-2003 (Rel. 75,

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RESULT 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1115 AGACAAAGGAGAGGAGGAATACCAGGCACGCTACAGAAGTGATCCAAATCTGGCCCGG 1174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1175 TATCCCGTAAAGCCACAACCCTACGAAGAACAAATGCGCATCCACGCTGAGGTGTCCAGG 1234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GCACGACATGAGAGAGACACAGTGATGTTTTTTTGGCAAACGCTGAACTAGAAGATTCC 1294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1295 AGGATTCTCTGCTAAGGATGGATAGACCATCAAGGCAAAGATCTGTATCTGAAGGTAGA 1354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1355 GCTGCAATGGAAAACCAACGATCGTATTCAATGGAAAGAACTCGAGAGGCTCAGGGACAA 1414
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                                                                                                                                                                                                                                                                      GAGAAAGGCCGAGCTCATGGGCTCACAAGACAGGATACTATTAAAAATGGATCAGGAGTG 814
                                                                                                                                                                                                                                                                                                   GACAAAAACAGATCTCAAGGACTCACCAGGCAAGACTCAATTAAGAATGGTTCTGGAGTA 121
                                                                                                                                                                                                                                                                                                                                                    AAGCACCAGATTGCCAGTGACATGCCTTCAGACAGAAAACGAAGTCCATCAGTGTCCAGG 874
                                                                                                                                                                                                                                                                                                                                                                          182 GAACAGAACAGAAGATACGACCAAAGGGAAGAGAGAGAAGAAGATATTCACAGTATGCTACA 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             935 TCAGATGGTACAATGCCAAGATCTCCTTCGGATTATGCTGATAGACGATCTCAGCGTGAG 994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              362 AGGCGTTCCAAGGAGTATCCGGTAGAAGAGAGGATGCACAGAACAGGAAGAAGAATATGAA 421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     302 CCTCAGTTATACGAAGAGCCTGAACTGGGTGATTATAGAGATTCCAACAGGAGGAGTGGC 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       601
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Ligate in double stranded adaptor containing Begl and BamHi sites [5/9gcogcgtgcagccccggatccgaaaaaag] [5/aattcttttttcggatccgggctgcacgc] [5/aattctttttcggatccggggctgcacgc] [7] 212 c 236 g 175 t
                                                                                                                                                                                                                        AGCTCCCAAGAGCATTTGCAGTACCAAGACCACCAGGTGACATATCCACACAG-TTTG
                                                                                                                                                                                             AAACTACACGAGCAGCCCCAGTTCCAAGGAGCCCCCAGGTGACTTATCAGTACCTGCAGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            602 CGGATATCTATGCTGAGGATGGAACGGCCGTCAAGGCAAAGATCGGTGTCTGAGGCGCAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1474 ACCGCTTGATAGACCAGACA-TGAGGCGCCTGACTCCCTACGGAAACAGCACCACTTAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            782 TCCTCTGGAAAGACCGGACATTGAGGCGCTCTGATTCATTAAGAAACAACAACATTTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4; Gaps
                                                                                                            Query Match

10.8%; Score 537.6; DB 13; Length 944;
Best Local Similarity 76.8%; Pred. No. 3e-102;
Matches 707; Conservative 0; Mismatches 209; Indels 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1592 GATTCTTTGAGTTCAGACCA 1611
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Homo sapiens (human)
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia;
Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1. .603

/db xref="taxon:9606"
/db xref="taxon:9606"
/db xref="mana"
/organism="Hone sapiens"
/clone="DKFZp686F14203"
/clone="DKFZp686F14203"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4430
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        544
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CCAAGACACTGCCAGCACGGTATGTAAAAGTGTATCTATTAGATAAGGGAGTCTGCATAG 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     603 GCTIGGCCTCTGATAGCCAGTTCAGTGATTTCCTGGATGGCCTTGGCCCTGCTCAGCTAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4251 GCCTGGCCTCTGACAGCCAGTTCAGTGATTTCCTGGATGGCCTGGGCCCTGGCTCAGCTAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4371 AAAAGGGACAGCTGGAGGTAGAAATCATCCGGGGCGCGCGGGCCTTGTGGGRAAACCAGGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                59; Indels 3; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1-603
Ansorge W., Krieger S., Regiert T., Rittmueller C., Schwager B.,
Mewes H.W., Weil B., Amid C., Osanger A., Fobo G., Han M., Wiemann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de; sequenced by EMBL (European Molecular Biology Laboratories, Heidelberg/Germanny) within the CDNA sequencing consortium of the German Genome Project.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            rl sequence also avaijable.
This clone (DKPZp686F14203) is available at the RZFD in Berlin.
Please contact the RZFD: Ressourcentrum, Heubnerweg 6,
14059 Berlin-Charlottenburg, GRRMANY; Email: clone@rzpd.de
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
9.9%; Score 493.8; DB 2; Length 603;
Best Local Similarity 89.7%; Pred. No. 4.5e-93;
Matches 541; Conservative 0; Mismatches 59; Indels 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (07-MAY-2003) to the EMBL/GenBank/DDBJ databases MIPS, Ingolstaedter Landstr.1, D-85764 Neuherberg, GERMANY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 603 BP; 145 A; 137 C; 138 G; 181 T; 2 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This is the 3' sequence of the clone insert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                             EST; expressed sequence tag.
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4080 GCCAAACCGAAGGAGGAGGTAAAAAGCTACGGAGCACTGTTCAGAGAAGCACGGAGGACCG 4139
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                                                                                                                                                                                                                                                                                                                         1140 GGCTAGCAGTGGAGATGAGGAACTGGATGACCCGGCCAGGCCGGGAATCCACAGATG 4199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4260 CTGACAGCCAGTTCAGTGATTTCCTGGATGGCCTGGGCCCTGCTCAGCTAGTGGGACGCC 4319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4320 AGACCCTGGCTACTCCTGCAATGGGTGACATTCAGGTGGGAATGATGGATAAAAAGGGAC 4379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4380 AGCTGGAGGTAGAAATCATCCGGGCGCGCGCGTTGTGGTAAAACCAGGTTCCAAGACA 4439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EST 09-0CT-2002
149 TGACAAAAGCACCAGCATCAGTGAGAGATGT-CGTACTGGAGAAAGAATGATGGCAGCC 207
                                                                                                                                                                                                         327
                                                                                                                                                                                                                                                                   508 CTGATAGCCAGTTCAGTGATTTCCTGGATGGCCTTGGCCTCTGCTCAGCTAGTGGGACGCC 567
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Tal: 319 335 8260

Fax: 319 335 8260

Exa: 319 335 8265

Exa: 319 335 9655

Email: bento-soares@uiowa.edu

Tissue Procurement: Dr. Gregg Hageman

CDNA Library preparation: Dr. M. Bento Soares, University of Iowa

CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa

CDNA Eibrary Arrayed by: Dr. M. Bento Soares, University of Iowa

Clone Distribution: Researchers may obtain clones from Research

Seq primer: M13 FORWARD
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Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene
                                                                   3960 AGTCCGACACTGCAGTGGGCCCCTGGGTACCAGTAGGAAGAGAGGGGGGATCTAGCATTG
                                                                                                         208 AGICTGACACTGCAGTGGGCACCTTGGGCACCAGTGGCAAAAAGCGGGGCCTTTGCCTTG
                                                                                                                                                                                         268 GTGCCAAAATGGTAGCTATCGTTGGTCTGTCAGGAAAAGTCGCAAGTGCTTCTCAGCTCA
                                                                                                                                                                                                                                                                                                                                                                                                                4200 GCAGCATGAACAGCTATAGCTCGGAAGGAAATCTGATCTTCCCTGGGGTCCGCCTGGCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   UI-E-CL1-aen-b-01-0-UI.sl UI-E-CL1 Homo sapiens CDNA clone UI-E-CL1-aen-b-01-0-UI 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Soares, MB
Coordinated Laboratory for Computational Genomics
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Genome Res. 6 (9), 791-806 (1996)
97044477
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (Dases 1 to 697)
Ma'Y., Qi,X., Zhang,X., Xiao,H., Zhu,Z., Yan,Q., Chen,Z. and Han,Z.
Petal Pituitary ESTs
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                                                            363 CCAAAAAGAAAACAAAAGIGGCAAGAAAAAGGCIGGAACCCCITTACCAGCAGCIATITAT 304
                                                                                                                          303 CITICGAAGAGGICCACAAGGAAAGITITACAGAICAICGICIGGGGGGGAGAITAIGGGC 244
                                                                                                                                                                                                               243 GCATGGATCACAAAINTTTTATGGAAGTGGCCCAGATACTTTTAGATGAACTAGAGCTAT 184
                                                                                                                                                                                                                                                                                                    89 ATACCAGTGTCTTTACATCCAAAATGCAAAGCAAATGGGCCATATCAGGGAAGAACA 148
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Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
Tel: 86-21-50801999 (ex.45)
                                                                                                                                                                                                                                                                                                                                                                                         123 TGGCCCCTCTGACAAGAGAGTTCCCAATCATCTGGAAAGTTCAATCTTCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            63 ACTCTCGTTCATAGCAGCTGTAAAAATTGTTGTCACAGCAACCAGCGTTACAAAAAA
                                                                                                  1551 CCTTCGAGGAGAGCCCCCAGGGAAGGGTGTTACAGATCATTGTCTGGGGAGATTATGGTC
                                                                                                                                                                                         GTATGGATCAAAATCCTTTATGGGAGTGGCCCAGATACTCTTAGATGAACTGGAACTAT
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9.8%; Score 487.8; DB 14; Length 697;
Best Local Similarity 89.5%; Pred. No. 8.3e-92;
Matches 547; Conservative 0; Mismatches 62; Indels 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CD237320 697 bp mRNA line
FNPAJEO4 FNP Homo sapiens CDNA, mRNA sequence.
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/db_xref="taxon:9606"
/tissue_type="pituitary"
/dev_stage="fetal"
/clone_lib="RNP"
/note="Vector: pTriplEx2; S:
a 150 c 201 g 126 t
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Bukaryofa, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Mammalia; Eutheria, Primates; Catarrhini, Hominidae, Bomo.

1 (Dases I to 590)

1 (Dases I to 590)

Rucaba, T., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J., Moore, B., Schallenberg, K., Steptoe, M., Tan, F., Theising, B., White, Y., Wylie, T., Washd-Marck EST Project 1997,

Unpublished
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                                                                                       590 bp mRNA linear EST 08-AUG-1997
IMPGE:784752 5' SIMILAR OWF:T10A3.I CE04931 C2 DOMAIN OF PROTEIN
AA476826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            65 TAGGAATGATGACAAAAAAGGCACAGCTGGAGGAAATCATCCGGGCCCG-TGCCTTG 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           124 TTGTAAAACCAGGTTCCAAGACACTGCCAGCACCGTATGTAAAAGTGTATCTATTAGATA 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: estewatson.wustl.edu
This clone is available royalty-free through LLWL; contact the
IWAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -28mil rev2 Fr from Amersham
High quality sequence stop: 495.
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9.0%; Score 446.4; DB 9; Length 590;
Best Local Similarity 89.4%; Pred. No. 4.1e-83;
Matches 504; Conservative 0; Mismatches 56; Indels 4; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
TEL: 314 286 1800
Fax: 314 286 1810
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /mol_type="mRNA"
/db_xref="GDB:5982370"
/db_xref="taxon:9606"
/clone="IMAGE:784752"
/dev stage="8-9 weeks"
/lab_host="DH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       organism∝"Homo sapiens"
27 ACCAGCGTTACAAAAAAAAAA 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       129 g
                                                                                                                                                                                                                  AA476826.1 GI:2205037
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Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4533 TOTACCAGCAGCTCTTGTCCTTCGAGGAGAGCCCCCCAGGGGAGGGTGTTACAGATCATTG 4592
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4593 TCTGGGGAGATTATGGTCGTATGGATCACAAATCCTTTATGGGAGTGGCCCCAGATACTCT 4652
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4773 GITCIACCGGACCTICITACTCTCGTTCATAGCAACT---ATAAAACTGTTGTCACAACA 4829
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                447 TIGITIGIAAAAACCAGGITCCAAGACACTGCCAGCACCGTATGTAAAAGTGTATCTATTAG 388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            387 ATAACGGAGTCTGCATAGCCAAAAGAAAACAAAAGTGGCAAGAAAAACGCTGGAACCC 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                207 TAGATGAACTAGAGCTATCCAATATGGTGATGGGTGGTTCAAACTTTTCCCACCTTCCT 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           567 troccicciócricaderadodacaccadaereridacaacacciócaaradaradarité 508
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Best Local Similarity 89.4%; Pred. No. 6.2e-86;
Matches 507; Conservative 0; Mismatches 57; Indels 3; Gaps
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                                                             'organism="Homo sapiens"
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Search completed: December 11, 2003, 23:10:52 Job time : 8950 secs